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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 264.331 Seconds
(without alignments)
5365.716 Million cell updates/sec

Title: US-09-300-482-1

Perfect score: 233

Sequence: 1 gtttttcagcttagtagaat.....ttgacaagggtatttcttg 233

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	233	100.0	233	US-09-237-183A-1252	Sequence 1252, Ap
2	221.8	95.2	2311	US-10-425-115-160360	Sequence 160360,
3	208.8	89.6	1770	US-10-425-115-160357	Sequence 160357,
4	164.8	70.7	1693	US-10-437-963-23894	Sequence 23894, A
5	164.8	70.7	5580	US-10-437-963-91761	Sequence 91761, A
6	141	60.5	749	US-10-425-115-174626	Sequence 174626,
7	138	59.2	713	US-10-767-701-12821	Sequence 12821, A
8	138	59.2	1929	US-10-425-115-48185	Sequence 48185, A
9	131.6	48.7	1924	US-10-739-930-5153	Sequence 5153, Ap
10	113.4	48.7	1900	US-10-437-963-509	Sequence 509, App
11	113.4	48.7	2583	US-10-437-963-508	Sequence 508, App

12	100.2	43.0	1844	17	US-10-425-114-9043	Sequence 9043, Ap
13	100.2	43.0	1854	17	US-10-425-114-29479	Sequence 29479, A
14	100.2	43.0	1947	17	US-10-424-599-81077	Sequence 81077, A
15	91.6	39.3	612	18	US-10-425-115-142724	Sequence 142724, A
16	87.2	37.4	2412	17	US-10-425-114-12043	Sequence 12043, A
17	87.2	37.4	2435	17	US-10-424-599-81074	Sequence 81074, A
18	82.2	35.3	1236	17	US-10-425-114-5220	Sequence 5220, Ap
19	82	35.2	666	18	US-10-767-701-10807	Sequence 10807, A
20	60.4	25.9	626	18	US-10-437-963-83072	Sequence 83072, A
21	42.8	18.4	105	18	US-10-425-115-60567	Sequence 60567, A
22	39	16.7	340	17	US-10-424-599-83608	Sequence 83608, A
23	35	15.0	402850	10	US-09-844-653-5	Sequence 5, Appl
24	34.6	14.8	672	17	US-10-282-122A-34479	Sequence 34479, A
25	34.4	14.8	10286	14	US-10-239-676-13	Sequence 13, Appl
26	34.4	14.8	10286	15	US-10-240-453-21	Sequence 21, Appl
27	34	14.6	649	13	US-10-027-632-139078	Sequence 139078,
28	34	14.6	649	17	US-10-027-632-139078	Sequence 139078,
29	33.6	14.4	23695	18	US-10-781-362-13	Sequence 13, Appl
30	33.6	14.4	23702	18	US-10-781-362-9	Sequence 9, Appl
31	33.6	14.4	23702	18	US-10-781-362-11	Sequence 11, Appl
32	33.6	14.4	23702	18	US-10-781-362-5	Sequence 5, Appl
33	33.6	14.4	23703	18	US-10-781-362-7	Sequence 7, Appl
34	33.6	14.4	23703	18	US-10-781-362-15	Sequence 15, Appl
35	33.6	14.4	23703	18	US-10-781-362-17	Sequence 17, Appl
36	33.6	14.4	23703	18	US-10-781-362-19	Sequence 19, Appl
37	32.4	13.9	233	18	US-10-425-115-172445	Sequence 172445,
38	32.4	13.9	241	18	US-10-674-124A-23429	Sequence 23429, A
39	32.4	13.9	649	13	US-10-027-632-139077	Sequence 139077,
40	32.4	13.9	649	17	US-10-027-632-139077	Sequence 139077,
41	31.4	13.5	234	17	US-10-424-599-7634	Sequence 7634, Ap
42	31.4	13.5	13376	15	US-10-311-455-556	Sequence 556, App
43	31.2	13.4	454	10	US-09-918-995-29025	Sequence 29025, A
44	31.2	13.4	472	13	US-10-027-632-40743	Sequence 40743, A
45	31.2	13.4	472	17	US-10-027-632-40743	Sequence 40743, A

ALIGNMENTS

RESULT 1
US-09-237-183A-1252
; Sequence 1252, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; PRIOR FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 1252
; LENGTH: 233
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-1252

Query Match 100.0%; Score 233; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 6.4e-66;
Matches 233; Conservative 0; Indels 0; Gaps 0;
QY 1 GTTTTTCAGCTTAGTAGAATATGATGAGCTCTATGATAGGCTGGAAGATTGACTT 60
DB 1 GTTTTTCAGCTTAGTAGAATATGATGAGCTCTATGATAGGCTGGAAGATTGACTT 60
QY 61 ATTGAATGAGCAATCTGAGTATGAGACTTCAGAAAAAATGACTGCGGAGCTACCG 120
DB 61 ATTGAATGAGCAATCTGAGTATGAGACTTCAGAAAAAATGACTGCGGAGCTACCG 120


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Db      1132 TCATCTGATGATTAATTCATCTTCTCATCTGCGTGAGCAAGGGTTATTGTTG 1183

RESULT 5
US-10-437-963-91761
/ Sequence 91761, Application US/10437963
/ Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Mu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 91761
LENGTH: 5580
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_90304C.1
US-10-437-963-91761

Query Match      70.7%; Score 164.8; DB 18; Length 5580;
Beet Local Similarity 81.9%; Pred. No. 5,9e-43;
Matches 190; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY      2 TTTTGGCAGTTAGTGAATATGTTAGTGCTCCTATGATGAGGTGGAAGATTGAGTTA 61
Db      4117 TTTTGGCATTATTAATTAATATGTTAGTGTGTTCTTCAATATGCGGGAAGATTGGCATCA 4176

QY      62 TTGAATGAGGCAATCTCTAGTATGAGACTTCAGAAAACAATGAATCTGGGAAGCTACCGC 121
Db      4177 TTAATAAGCCATTTCAGAGATGAATGAATCTTGAGAAACAACAACAGAGAGCTCAGT 4236

QY      122 AGATTATTTTATTTGGCATTGCTCCATCATGCTTACCATCATGATATCGAGATATAGA 181
Db      4237 AGACATTTTATTTGGCATTGCTCCATCATGCTTACCATCCCCCAGATGCAAAATGATAGA 4296

QY      182 TCATATGTCATAGTGCATCTTCACACACCGGTGGACAAGGGTTATTGTTG 233
Db      4297 TCATCTGATGATTAATTCATCTTCTCATCTGCGTGAGCAAGGGTTATTGTTG 4348

RESULT 6
US-10-425-115-174626
/ Sequence 174626, Application US/10425115
/ Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 174626
LENGTH: 749
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_9083C.1
US-10-425-115-174626

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Query Match      60.5%; Score 141; DB 18; Length 749;
Best Local Similarity 80.5%; Pred. No. 1.5e-35;
Matches 165; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy      2      TTTTGGCAGTTAGTAGAATATGTTAGTGGCTCTCATATGATAGAGGTGGAAGATTGAGTTA 61
Db      545     TTTTGGCAATTAATTAAGTATGATGTGTTCCATATGATTAATGGGGCAGGATTTGAAATTG 604

Qy      62      TTGAATGAGGCAATCTCTGAGTATGAGACTTCAGAAAACATGACTCGGGAAGCTAACGCC 121
Db      605     CTAAACAAGAACAACTCTGAGAAATGAAACATCAGAGAACCAACACAGGAAACTCCCGA 664

Qy      122     AGATTATTTTATTTTGGCATTGCTCCATCAGCTCTACCCATCAGATGAGATGATGATTAAGA 181
Db      665     AGACTATTTTATTTTGGCATTACCTCTTCAATGTATACCCCTCAGTATGCAAAATGATTAAGA 724

Qy      182     TCATATTTGCATGAGTCATCTTTCAC 206
Db      725     TCATATTTGCATGAGTCATCTTCTTC 749

RESULT 7
US-10-767-701-12821
; Sequence 12821, Application US/107677701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 12821
; LENGTH: 713
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAV03-CLUS32515_1
US-10-767-701-12821

Query Match      59.2%; Score 138; DB 18; Length 713;
Best Local Similarity 78.0%; Pred. No. 1.4e-34;
Matches 181; Conservative 0; Mismatches 45; Indels 6; Gaps 1;

Qy      2      TTTTGGCAGTTAGTAGAATATGTTAGTGGCTCTCATATGATAGGGTGAAGATTGAGTTA 61
Db      390     TTTTGGCAATTAATTAAGTATGATGTGCTGTTCTCATGACACTGAGGAAGATTTCAGAAA 449

Qy      62      TTGAATGAGGCAATCTCTGAGTATGAGACTTCAGAAAACATGACTCGGGAAGCTAACGCC 121
Db      450     CTGAACAAGAACAAATATCAAGATAGAGGCGTCA-----AACAAATCAGGAAGCTATFCGC 503

Qy      122     AGATTATTTTATTTTGGCATTGCTCCATCAGCTCTACCCATCAGATGAGATGATGATTAAGA 181
Db      504     AGGCTCTTTTATTTTGGCATTGCTCCATCTGTCTTACCTTTCAGTGTGCAAAATGATCAGA 563

Qy      182     TCATATTTGCATGAGTCATCTTTCACACACCGGTTGAGACAAGGTTATTTGTTG 233
Db      564     ACATATTTGCATGAGTCCATCTTCTCACCCCTGGATGAGACAGAGTATTTGTTG 615

RESULT 8
US-10-425-115-48185
; Sequence 48185, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425.115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 48185
LENGTH: 1929
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_143951C.1
US-10-425-115-48185

Query Match 59.2%; Score 138; DB 18; Length 1929;
Best Local Similarity 78.0%; Pred. No. 2.2e-34;
Matches 181; Conservative 0; Mismatches 45; Indels 6; Gaps 1;

QY 2 TTTTTCAGTTAGTATAGTATAGTGGCTCCATATAGGCTGGAGAGATTGAGTTA 61
DB 497 TTTTTCAGTTAGTATAGTATAGTGGCTCCATATAGGCTGGAGAGATTGAGTTA 556
QY 62 TTGAATGAGCAATCTCTGAGTATGAGACTTCAGAAAACAATGACTCGGAGCTACCGC 121
DB 557 CTGAACAGGGCAATATCAGATATGAGGTGCA-----AAGGTTGAGAGACTATCCG 610
QY 122 AGATTATTTATTTGGCATGCTCCATCATCTACCTACCATCATATGCGATGATTAAGA 181
DB 611 AGGCTCTTTATTTGGCATGCTCCATCATCTACCTACCATCATATGCGAAATGATCAGA 670
QY 182 TCATATTGATGATGATTCATCTTACACACCGGTTGACAAAGGTTATTGTTG 233
DB 671 ACATATTGATGATGATTCATCTTCTCAOCCGATGATGACAGATCATTTGTTG 722

RESULT 9
US-10-739-930-5153
Sequence 5153, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
FILE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 5153
LENGTH: 1924
TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER606_35
US-10-739-930-5153

Query Match 56.5%; Score 131.6; DB 18; Length 1924;
Best Local Similarity 76.3%; Pred. No. 2.8e-32;
Matches 177; Conservative 0; Mismatches 49; Indels 6; Gaps 1;

QY 2 TTTTTCAGTTAGTATAGTATAGTGGCTCCATATAGGCTGGAGAGATTGAGTTA 61
DB 455 TTTTTCAGTTAGTATAGTATAGTGGCTCCATATAGGCTGGAGAGATTGAGTTA 514
QY 62 TTGAATGAGCAATCTCTGAGTATGAGACTTCAGAAAACAATGACTCGGAGAGCTACCGC 121
DB 515 CTGAACAGGGAAATATCAGATATGAGGTGCA-----AACAATGAGAGAGCTCCCGT 568
QY 122 AGATTATTTATTTGGCATGCTCCATCATCTACCTACCATCATATGCGATGATTAAGA 181
DB 569 AGGCTCTTTATTTGGCATGCTCCATCATCTACCTACCATCATATGCGAAATGATCAGA 628
QY 182 TCATATTGATGATGATTCATCTTACACACCGGTTGACAAAGGTTATTGTTG 233

DB 629 ACATATTGATGATGATTCATCTTCTCAOCCGATGATGACAGATCATTTGTTG 680

RESULT 10
US-10-437-963-509
Sequence 509, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 509
LENGTH: 1900
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)-(1900)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: PAT_MRT4530_100464C.1
US-10-437-963-509

Query Match 48.7%; Score 113.4; DB 18; Length 1900;
Best Local Similarity 75.1%; Pred. No. 2.5e-26;
Matches 157; Conservative 0; Mismatches 46; Indels 6; Gaps 1;

QY 2 TTTTTCAGTTAGTATAGTATAGTGGCTCCATATAGGCTGGAGAGATTGAGTTA 61
DB 442 TTTTTCAGTTAGTATAGTATAGTGGCTCCATATAGGCTGGAGAGATTGAGTTA 501
QY 62 TTGAATGAGCAATCTCTGAGTATGAGACTTCAGAAAACAATGACTCGGAGAGCTACCGC 121
DB 502 TTGAACAGGGAAATTTGAGATATGAGAGTCA-----AACAATGAGAGAGCTCCCGC 555
QY 122 AGATTATTTATTTGGCATGCTCCATCATCTACCTACCATCATATGCGATGATTAAGA 181
DB 556 AGGCTCTTTATTTGGCATGCTCCATCATCTACCTACCATCATATGCGAAATGATCAGA 615
QY 182 TCATATTGATGATGATTCATCTTACACAC 210
DB 616 ACATATTGATGATGATTCATCTTCTCAOCCGATGATGAC 644

RESULT 11
US-10-437-963-508
Sequence 508, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 508
 LENGTH: 2583
 TYPE: DNA
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_100463C.1
 US-10-437-963-508

Query Match 48.7%; Score 113.4; DB 18; Length 2583;
 Best Local Similarity 75.1%; Pred. No. 2.9e-26;
 Matches 157; Conservative 0; Mismatches 46; Indels 6; Gaps 1;

Db 1453 TTTTGGCAACATATATATATATGTCAGTGGTCTTATGACGCGGAGAAAGATTGAGAAA 1512
 Qy 2 TTTTGGCACTAGTATGATATATGTTAGTGGCTCTTATGATAGGTTGAGAGATTGAGTTA 61
 Db 62 TTGAATGAGGCAATCTCTGAGATAGAGACTTCAGAAAACAATGACTCGGGAAGCTACCGC 121
 1513 TTGAACAAGGAATTTCAAGATAGAGAGTCA-----AACAAATCAGAAAAGCCCTCGC 1566
 Qy 122 AGATTATTTTATTTGGCATTTGGCTCCATCATCTACCCATCCATGATGCGAGATGATAGA 181
 1567 AGGCTCTTCTATTTGGCATTTGGCTCCATCTCTACCTTCACTGCTGCAAAATGATCAGA 1626
 Db 182 TCATATTTGCATGAGTTCATCTTTCACACAC 210
 1627 ACATATTCATGATGATTCATCTGATGAGAC 1655

RESULT 12
 US-10-425-114-9043

; Sequence 9043, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 9043
 ; LENGTH: 1844
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700832220_FLI
 US-10-425-114-9043

Query Match 43.0%; Score 100.2; DB 17; Length 1844;
 Best Local Similarity 64.4%; Pred. No. 5.3e-22;
 Matches 150; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 1 GTTTTTCAGTTAGTATGATATGTTAGTGGCTCTTATGATAGGTTGGAAGATTGAGTT 60
 Db 400 GTTTTTCAGCTGATCAATAATGTAAGCGGCTCTTATGATTCGAGATAGGCTTCGCGCT 459
 Qy 61 ATTGAATGAGCAATCTCTGAGATAGAGACTTCAGAAAACAATGACTCGGGAAGCTACCG 120
 Db 460 GTTGGATTAAGAGATTTCAAGAGATTAATTTGAAAAACAGTGTGAGAGGTTTATCTCG 519
 Qy 121 CAGATTATTTTATTTGGCATTTGGCTCCATCATCTACCCATCCATGATGCGAGATGATAAG 180
 Db 520 GAGGCTTTTCTATCTTCTGCTTTCACCTTCAGATATTCATCATGATTGCAAGATGATCA 579
 Qy 181 ATCATATTCATGATGATTCATCTTTCACACACCGGTTGAGACAGGTTATTTGTTG 233

Db 580 GACTTGTTCATGATTAATCTGATCTTGTGATGAGACACGCGTTGTTG 632

RESULT 13

US-10-425-114-29479
 ; Sequence 29479, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 29479
 ; LENGTH: 1854
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-GMFLMINSOY050C02_FLI
 US-10-425-114-29479

Query Match 43.0%; Score 100.2; DB 17; Length 1854;
 Best Local Similarity 64.4%; Pred. No. 5.3e-22;
 Matches 150; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 1 GTTTTTCAGTTAGTATGATATGTTAGTGGCTCTTATGATAGGTTGGAAGATTGAGTT 60
 Db 410 GTTTTTCAGCTGATCAATAATGTAAGCGGCTCTTATGATTCGAGATAGGCTTCGCGCT 469
 Qy 61 ATTGAATGAGCAATCTCTGAGATAGAGACTTCAGAAAACAATGACTCGGGAAGCTACCG 120
 Db 470 GTTGGATTAAGAGATTTCAAGAGATTAATTTGAAAAACAGTGTGAGAGGTTTATCTCG 529
 Qy 121 CAGATTATTTTATTTGGCATTTGGCTCCATCATCTACCCATCCATGATGCGAGATGATAAG 180
 Db 530 GAGGCTTTTCTATCTTCTGCTTTCACCTTCAGATATTCATCATGATTGCAAGATGATCA 589
 Qy 181 ATCATATTCATGATGATTCATCTTTCACACACCGGTTGAGACAGGTTATTTGTTG 233
 Db 590 GACTTGTTCATGATTAATCTGATCTTGTGATGAGACACGTTGTTGTTG 642

RESULT 14
 US-10-424-599-81077

; Sequence 81077, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J
 ; APPLICANT: Kovalic, David K
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 81077
 ; LENGTH: 1947
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_44228C.1
 US-10-424-599-81077

Query Match 43.0%; Score 100.2; DB 17; Length 1947;
Best Local Similarity 64.4%; Pred. No. 5.4e-22;
Matches 150; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

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QY 1 GTTTTGCACTTAGTAAATATGTTAGTGGCTCTCTATGATAGGGTGAAGATTGGATT 60
    |||||
Db 481 GTTTTACAGCTGATCAATATATGTAAGCGGCTCTTATGATTCGAGGATGGCTCCGCT 540
    |||||
QY 61 ATTGAATGAGGCATCTCTAGATATGAGACTTCAGAAAACAATGACTCGGGAAGTACCG 120
    |||||
Db 541 GTTGGATMAAGAGATTCAAGCATGAATATTGAAAAACAGTTTGAGGGTTATCTCG 600
    |||||
QY 121 CAGATTATTTTATTTGGCATTTGCTCCATCGTCTACCCATGATGCGATGATGAATAG 180
    |||||
Db 601 GAGGCTTTTCTATCTGCTCTTCCACCTTCAAGTATATCCATCAGTTTGCAAGATGACA 660
    |||||
QY 181 ATCAATATTCATAGATTCATCTTCAACACCGGTTGACAGAGGTTATTTGTTG 233
    |||||
Db 661 GACTGTGTGATGAATAAATCTGATCTTGGTGGATGAGACGTTGTTGTTG 713
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RESULT 15

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US-10-425-115-142724
; Sequence 142724, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 142724
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_61645C.1
US-10-425-115-142724
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Query Match 39.3%; Score 91.6; DB 18; Length 612;
Best Local Similarity 74.4%; Pred. No. 2.1e-19;
Matches 131; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

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QY 2 TTTTTCAGTATGATATATGTAGTGGCTCTATGATAGGGTGAAGATTGGATT 61
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Db 440 TTCTTGCAATTGATATAATATATGTCAGTGGTCTCTATGACGCGAAGAAAGTTGAAAA 499
    |||||
QY 62 TTGAATGAGGCATCTCTGAGATATGAGACTTCAGAAAACAATGACTCGGGAAGTACCGC 121
    |||||
Db 500 CTGAACAAAGAAATATCAGATTATGAGATGTC-----CAACAACCTCGGGAATCTCCGC 553
    |||||
QY 122 AGATTATTTTATTTGGCATTTGCTCCATCAGTCTACCCATCAGTATGCGAGATGAT 177
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Db 554 AGGCTATTTTATTTGGCATTTGCTCCATCAGTCTTACCTTCACTGGCAAAATGAT 609
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Search completed: May 4, 2005, 21:11:26
Job time : 266.351 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 76.9588 Seconds
(without alignments)
5591.830 Million cell updates/sec

Title: US-09-300-482-4

Perfect score: 263
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61.4	23.3	1830121	4 US-09-557-884-1	Sequence 1, Appli
2	61.4	23.3	1830121	4 US-09-643-990A-1	Sequence 1, Appli
3	59.6	22.7	6132	4 US-09-809-665A-7	Sequence 7, Appli
4	58.2	22.1	1533	4 US-09-134-000C-2369	Sequence 2369, Ap
5	54	20.5	3015	4 US-09-710-279-3401	Sequence 3401, Ap
6	54	20.5	3081	4 US-09-710-279-3602	Sequence 3602, Ap
7	52	19.8	1548	4 US-09-107-532A-1949	Sequence 1949, Ap
8	51.4	19.5	16392	4 US-08-956-121E-53	Sequence 53, Appli
9	51.4	19.5	16392	4 US-08-781-986A-53	Sequence 53, Appli
10	50.6	19.2	2494	3 US-08-714-918-3	Sequence 3, Appli
11	50.6	19.2	2494	3 US-09-265-315-3	Sequence 3, Appli
12	50.6	19.2	2494	3 US-09-265-315-3	Sequence 3, Appli
13	50.6	19.2	2494	3 US-09-266-417-3	Sequence 3, Appli
14	50.6	19.2	2494	3 US-09-527-745-3	Sequence 3, Appli
15	50.6	19.2	2494	3 US-09-527-745-3	Sequence 3, Appli
16	49.6	18.9	1488	3 US-08-962-859A-1	Sequence 1, Appli
17	49.6	18.9	1488	4 US-09-583-110-1905	Sequence 1905, Ap
18	49.6	18.9	1488	4 US-09-107-433-785	Sequence 785, App
19	49	18.6	669	4 US-09-902-540-1996	Sequence 1996, Ap
20	49	18.6	720	4 US-09-902-540-4	Sequence 4, Appli
21	48.2	18.3	744	4 US-09-248-796A-3185	Sequence 3185, Ap
22	48	18.3	2764	2 US-08-986-963-4	Sequence 4, Appli
23	48	18.3	13121	2 US-08-961-527-126	Sequence 126, App
24	47.2	17.9	640681	4 US-09-790-988-1	Sequence 1, Appli
25	45.2	17.2	1554	3 US-09-134-001C-351	Sequence 351, App
26	44.6	17.0	219	3 US-09-134-001C-1197	Sequence 1197, Ap
27	42.6	16.2	2631	4 US-09-949-016-4987	Sequence 4987, Ap

28	42	16.0	3376	4 US-09-710-279-4055	Sequence 4055, Ap
29	39.6	15.1	6995	4 US-09-531-265-1	Sequence 1, Appli
30	37.4	14.2	1461	3 US-08-445-463B-5	Sequence 5, Appli
31	37.4	14.2	1461	3 US-08-445-464C-5	Sequence 5, Appli
32	37.4	14.2	1461	3 US-08-044-857D-5	Sequence 5, Appli
33	37.4	14.2	1461	3 PCT-US94-03437-5	Sequence 5, Appli
34	37.2	14.1	1455	5 PCT-US94-03437-7	Sequence 7, Appli
35	37.2	14.1	1467	5 PCT-US94-03437-3	Sequence 3, Appli
36	37.2	14.1	1571	3 US-08-445-463B-3	Sequence 3, Appli
37	37.2	14.1	1571	3 US-08-445-464C-3	Sequence 3, Appli
38	37.2	14.1	1571	3 US-08-044-857D-3	Sequence 3, Appli
39	37.2	14.1	1696	1 US-07-737-071A-1	Sequence 1, Appli
40	37.2	14.1	1696	1 US-08-022-096-1	Sequence 1, Appli
41	37.2	14.1	1696	3 US-08-445-463B-7	Sequence 7, Appli
42	37.2	14.1	1696	3 US-08-445-464C-7	Sequence 7, Appli
43	37.2	14.1	1696	3 US-08-044-857D-7	Sequence 7, Appli
44	36.4	13.8	34266	4 US-09-949-016-13250	Sequence 13250, A
45	36.2	13.8	2853	4 US-09-620-312D-463	Sequence 463, App

ALIGNMENTS

RESULT 1
US-09-557-884-1/c
Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
Query Match 23.3%; Score 61.4; DB 4; Length 1830121;
Best Local Similarity 52.1%; Pred. No. 1.3e-08;
Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 53 AGGATGAGATGCAATATATTGAGAGCCATTGGCTTGATGACACTTTCTTCCCATTA 112

Db 577356 ATGGCTGAAAACGTTATTCGTTGAAAAACCTTTGGTTAGAGTAAAAACACGGCAAA 577297
Qy 113 GGCTGACAAATATCTTCTTTCAAACTTTCAGAAAAAGCAATATATAGATTGANCATC 172
Db 577296 CATTAAGCGTACAAATCCACCGTTCTTTGAAAGAACCAAAATTTATCGTATGATCAIT 577237
Qy 173 TACTAGAGAAGAAATCNCAGTAAATAATCCNAGGTTTAAGGTTTCAANNAGNTTTTG 232
Db 577236 ATTTAGGTAAAGAAACCGTTCAAAACTTGTCTGTAATTAAGTTTCAAAATGTTGTTTG 577177
Qy 233 AGCCACCTTNGAGNNGNACNTNNNNGANA 263
Db 577176 AACCGCTTGGAAACCGTAATTTCAATGATTA 577146

RESULT 2

US-09-643-990A-1/c
Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Pleischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS V6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match 23.3%; Score 61.4; DB 4; Length 1830121;
Best Local Similarity 52.1%; Pred. No. 1.3e-08;
Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
Qy 53 AGGATGGAATCGATATATTTGAGAGCCATTGGCTTGATGACATTTCTTCCATA 112

Db 577356 ATGGCTGAAAACGTTATTCGTTGAAAAACCTTTGGTTAGATGAAAAACACGGCAAA 577297
Qy 113 GGCTGACAAATATCTTCTTTCAAACTTTCAGAAAAAGCAATATATAGATTGANCATC 172
Db 577296 CATTAAGCGTACAAATCCACCGTTCTTTGAAAGAACCAAAATTTATCGTATGATCAIT 577237
Qy 173 TACTAGAGAAGAAATCNCAGTAAATAATCCNAGGTTTAAGGTTTCAANNAGNTTTTG 232
Db 577236 ATTTAGGTAAAGAAACCGTTCAAAACTTGTCTGTAATTAAGTTTCAAAATGTTGTTTG 577177
Qy 233 AGCCACCTTNGAGNNGNACNTNNNNGANA 263
Db 577176 AACCGCTTGGAAACCGTAATTTCAATGATTA 577146

RESULT 3

US-09-809-665A-7
Sequence 7, Application US/09809665A
Patent No. 6790950
GENERAL INFORMATION:
APPLICANT: Lowery E., David, et al.
TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
FILE REFERENCE: 28341/00435
CURRENT APPLICATION NUMBER: US/09/809,665A
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/153,453
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/126,689
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 09/545,199
NUMBER OF SEQ ID NOS: 2000-04-06
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH: 6132
TYPE: DNA
ORGANISM: Pasteurella multocida
FEATURE:
NAME/KEY: CDS
LOCATION: (4032)..(4727)
OTHER INFORMATION: devb
US-09-809-665A-7

Query Match 22.7%; Score 59.6; DB 4; Length 6132;
Best Local Similarity 51.4%; Pred. No. 3.5e-09;
Matches 110; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
Qy 50 AGAAGGATGGAATCGATATATTTGAGAGCCATTGGCTTGATGACATTTCTTCCC 109
Db 2903 AGTTGGCTGGAAGCGTTATTTGTGAAAAACCGTTTGGTTATGATATACGACGCA 2962
Qy 110 ATAGGCTGACAAATATCTTCTTTCAAACTTTCAGAAAAAGCAATATATAGATTGANC 169
Db 2963 AAGAATCTGATATTCAAATTCACCGTTCTTGTGATGAAACCAAAATTTATCGATTGACC 3022
Qy 170 ATCTACTAGAGAAGAAATCNCAGTAAATAATCCNAGGTTTAAGGTTTCAANNAGNTT 229
Db 3023 ACTATCTTGTGTAAGAAACCGTTCAAAATCTGCTGTGTGTTGCTTTTCTAATGATGCT 3082
Qy 230 TTGAGCCACCTTNGAGNNGNACNTNNNNGANA 263
Db 3083 TTGAACCACTCTGGAACCGTAATTTCAATGATTA 3116

RESULT 4

US-09-134-000C-2369
Sequence 2369, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arianello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1949:
SEQUENCE CHARACTERISTICS:
LENGTH: 1548 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...1548
SEQUENCE DESCRIPTION: SEQ ID NO: 1949:
US-09-107-532A-1949

Query Match 19.8%; Score 52; DB 4; Length 1548;
Best Local Similarity 48.3%; Pred. No. 5.9e-07;
Matches 112; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
QY 32 CAAGCAGTCTGACCCAGAGGATGATGATATATTTGAGAGCCATTGGCT 91
DB 419 CCAAAATATTTATGACAAAATGCTTCATGTTGATCATAGAAAACCGTTCGTT 478
QY 92 TTGATGACATTTCTCCCAATAGCTGACACATATTTCTTCAACCTTCAGAAAAGC 151
DB 479 CTGATTAACAGCTCTGTTTGAATGAAACCAATCAGAGAGTATCCAGAAACAAG 538
QY 152 AATATATATGAAATGATGATCTACTAGAAAGATCNCAGTNAATAATCCTNAGAGTTTAA 211
DB 539 ATATTTTTCAGATGATGATATTTTATTTAGAAAAGAAATGATCCAAACATCTTCAGCTATCC 598
QY 212 GGGTTTCAANNAGTTTTCAGCCACTTNGAGNNAGNCNTNNNNNGANNA 263
DB 599 GTTTGCCAATAATATTTTGAAGCTCAATGGAACAATCGTATATCGACA 650

RESULT 8

US-08-956-171E-53
Sequence 53, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 16592 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-08-956-171E-53

Query Match 19.5%; Score 51.4; DB 4; Length 16592;
Best Local Similarity 51.0%; Pred. No. 2.8e-06;
Matches 103; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 52 AAGGATGGAATCCCATATATTTGAGAGCCATTGGCTTGATGACATTTCTCCCAT 111
DB 814 AAGGATTTAAAGCCCTGTTATGAAAACCATTCGTAGTGAATTAATCAGCCGA 873
QY 112 AGCTGACACAATATCTTCTTCAACTTCAGAGAAAGCAATATATGAAATGANCAT 171
DB 874 GCATTAACAATCAATTCGTAATCATTTTAAAGAAAGAAATTTATCGATTTGACCAC 933
QY 172 CTACTAGAGAGAAATCNCAGTNAATAATCCTNAGGTTTAAAGGTTTCAANNAGTTTT 231
DB 934 TATTTAGAAAAGCATGTTCAAAATATCAGAGTATTAAGTTTGGCAATGGAGTTT 993
QY 232 GAGCCACTTNGAGNNAGNCNT 253
DB 994 GAACCATTAATGAAATACAAAT 1015

RESULT 9

US-08-781-986A-53
Sequence 53, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Bob
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PB248BP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16592 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-781-986A-53

Query Match 19.5%; Score 51.4; DB 4; Length 16592;
 Best Local Similarity 51.0%; Pred. No. 2.8e-06;
 Matches 103; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

52 AAGGATGGAATCGATATATTTGAGAGCCATTGGCTTGATGCACTTCTTCCAT 111
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 814 AAGGATTTAAACGCTGTATCGAAAAACATTGCGTAGTATTTAAATCAGCCGA 873
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 112 AGCGTACACATATCTTCTTCAACTTCAGSAAAGCAATATATGATGANCAT 171
 |||||
 874 GCATTAAACATCAATTCGTAATCATTTAAAGAAAGAAATTTATGATGACAC 933
 |||||
 172 CTACTAGGAGGATCNCAGTAAATCCTTCAGGTTTAAGGTTTCAANNAGTTT 231
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 934 TATTTAGGAAAGACATGTTTCAAAATATCGAGTATTTAGTTTCCGAAATCGATGTT 993
 |||||
 232 GAGCCACCTTGAGNNGNACNT 253
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 994 GAACCATTAATGAAATACAAAT 1015
 |||||

RESULT 10
 US-08-714-918-3/c
 ; Sequence 3, Application US/08714918
 ; Patent No. 6037123
 ; GENERAL INFORMATION:
 ; APPLICANT: Benton, Bret
 ; APPLICANT: Lee, Ving
 ; APPLICANT: Malouin, Francois
 ; APPLICANT: Martin, Patrick K.
 ; APPLICANT: Schmid, Molly B.
 ; APPLICANT: Sun, Dongxu
 ; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
 ; TITLE OF INVENTION: TARGET GENES
 ; NUMBER OF SEQUENCES: 111
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/714,918
 ; FILING DATE: September 13, 1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/009,102
 ; FILING DATE: December 22, 1995
 ; APPLICATION NUMBER: 60/003,798

FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 222/005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2494 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-714-918-3

Query Match 19.2%; Score 50.6; DB 3; Length 2494;
 Best Local Similarity 50.0%; Pred. No. 2.1e-06;
 Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

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 1365 GCATTAAACATCAATTCGTAATCATTTAAAGAAAGAAATTTATGATGACAC 1306
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 172 CTACTAGGAGGATCNCAGTAAATCCTTCAGGTTTAAGGTTTCAANNAGTTT 231
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 1305 TATTTAGGAAAGACATGTTTCAAAATATCGAGTATTTAGTTTCCGAAATCGATGTT 1246
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 232 GAGCCACCTTGAGNNGNACNT 253
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 1245 GAACCATTAATGAAATACAAAT 1224
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RESULT 11
 US-09-265-315-3/c
 ; Sequence 3, Application US/09265315
 ; Patent No. 6187541
 ; GENERAL INFORMATION:
 ; APPLICANT: Benton, Bret
 ; APPLICANT: Lee, Ving J.
 ; APPLICANT: Malouin, Francois
 ; APPLICANT: Martin, Patrick K.
 ; APPLICANT: Schmid, Molly B.
 ; APPLICANT: Sun, Dongxu
 ; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 ; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 ; NUMBER OF SEQUENCES: 111
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/265,315
 ; FILING DATE: March 9, 1999
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-3

Query Match 19.2%; Score 50.6; DB 3; Length 2494;
Best Local Similarity 50.0%; Pred. No. 2.1e-06;
Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

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QY 112 AGGCTGACACATATCTCTTTCAAACTTCAGAAAAACAATATATAGAAATTGANCAT 171
DB 1365 GCATTAAACAATCAATTCGTAATCATTTTAAAGAAAGAAATTAATGATKGCAC 1306
QY 172 CTACTAGGAAGAAATCNCAGTNAATCCTNCAGGTTTAAGGTTTCAANNAGTTT 231
DB 1305 TATTAGAAAAAGCATGTGTTCAAAATATCAGAGTATTACGTTTGCATGCGATGTT 1246
QY 233 GAGCCACCTTNGAGNNAGNCAT 253
DB 1245 GAACCATTAATGAATTAACAAT 1224

RESULT 12
US-09-265-315-3/c
Sequence 3, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315

FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-3

Query Match 19.2%; Score 50.6; DB 3; Length 2494;
Best Local Similarity 50.0%; Pred. No. 2.1e-06;
Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

QY 52 AAGGATGGAATGCCATTAATATTGAGAAAGCCATTGGCTTGATGCACTTTCTTCCCAT 111
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DB 1365 GCATTAAACAATCAATTCGTAATCATTTTAAAGAAAGAAATTAATGATKGCAC 1306
QY 172 CTACTAGGAAGAAATCNCAGTNAATCCTNCAGGTTTAAGGTTTCAANNAGTTT 231
DB 1305 TATTAGAAAAAGCATGTGTTCAAAATATCAGAGTATTACGTTTGCATGCGATGTT 1246
QY 233 GAGCCACCTTNGAGNNAGNCAT 253
DB 1245 GAACCATTAATGAATTAACAAT 1224

RESULT 13
US-09-266-417-3/c
Sequence 3, Application US/09266417
Patent No. 6228588
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible


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        SOFTWARE: Word Perfect 5.1
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        FILING DATE: March 9, 1999
        CLASSIFICATION: 435
        PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 08/714,918
        FILING DATE: September 13, 1996
        APPLICATION NUMBER: 60/009,102
        FILING DATE: December 22, 1995
        APPLICATION NUMBER: 60/003,798
        FILING DATE: September 15, 1995
        ATTORNEY/AGENT INFORMATION:
        NAME: Mabury, Richard J.
        REGISTRATION NUMBER: 32,337
        REFERENCE/DOCKET NUMBER: 240/248
        TELECOMMUNICATION INFORMATION:
        TELEPHONE: (213) 469-1600
        TELEFAX: (213) 955-0440
        TELEX: 67-3510
        INFORMATION FOR SEQ ID NO: 3:
        SEQUENCE CHARACTERISTICS:
        LENGTH: 2494 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
US-09-266-417-3

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1 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
2 storage
3 COMPUTER: IBM Compatible
4 OPERATING SYSTEM: IBM P.C. DOS 5.0
5 SOFTWARE: Word Perfect 5.1
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7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/09/528,709
9 FILING DATE: 17-Mar-2000
10 CLASSIFICATION: 424
11
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US/08/714,918
14 FILING DATE: September 13, 1996
15 APPLICATION NUMBER: 60/009,102
16 FILING DATE: December 22, 1995
17 APPLICATION NUMBER: 60/003,798
18 FILING DATE: September 15, 1995
19
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Warburg, Richard J.
22 REGISTRATION NUMBER: 32,327
23 REFERENCE/DOCKET NUMBER: 222/005
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (213) 489-1600
26 TELEFAX: (213) 955-0440
27
28 TELEX: 67-3510
29
30 INFORMATION FOR SEQ ID NO: 3:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 2494 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36
37 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
38
39 IS-09-528-709-3

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RESULT 14
 US-09-528-709-3/c
 Sequence 3, Application US/09528709
 Patent No. 6630303
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 Lee, Ving
 Malouin, Francois
 Martin, Patrick K.
 Schmid, Molly B.
 Sun, Dongxu
 TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
 TARGET GENES
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 312 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:

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Query Match      19.2%; Score 50.6; DB 4; Length 2494;
Best Local Similarity 50.0%; Pred. No. 2.1e-06;
Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

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Db       1425 AAAGATTTAAAGCGCTTGTTATGAAAAACAATCGGTAGTATTTAAATCAGCGGA 1366
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QY      112   AGCGTGACACAAATATCTTCTTTCAAACCTTTCAGAAAAGCAATATATAGAAATTGANCAT 171
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; Sequence 3, Application US/09527745
; Patent No. 6638718
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; Lee, Ying
; Malouin, Francois
; Martin, Patrick K.
; Schmid, Molly B.
; Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles

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STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/527,745
FILING DATE: 17-Mar-2000
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-527-745-3

Query Match      19.2%; Score 50.6; DB 4; Length 2494;
Best Local Similarity 50.0%; Pred. No. 2.1e-06;
Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

QY 52 AAGGATGGAATCGCATATATTTGGAAGCCATTGGCTTGATGCACTTCTTCCCAT 111
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DB 1425 AAGGATTTAAACGCTTGTTATCGAAAAACATTCGTAAGTATTAATCAAGCCGA 1366
   |||||

QY 112 AGGCTGACACATATCTTCTTCAAACTTCAGAAAAAGCAATATATAGATTGANCAT 171
   |||||
DB 1365 GCATTAAACAATCAATTCGTAATCATTTTAAAGAGAGANAATTTATCGTATKAGCCAC 1306
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QY 172 CTACTAGAGAGAAATCNCAGTNAAAATCCTTCAGGTTTAAGGTTTCAANNAGNTTTT 231
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QY 232 GAGCCACCTTNGANGNAGNCNT 253
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DB 1245 GAACCATTAATGAATAACAAT 1224
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Search completed: May 4, 2005, 12:27:36
Job time : 81.958 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 298.387 Seconds
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5365.716 Million cell updates/sec

Title: US-09-300-482-4
Perfect score: 263
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Scoring table: IDENTITY NUC
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Searched: 5642217 seqs, 3043843248 residues
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Listing first 45 summaries

Database : Published Applications NA:*

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- 22: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	175.8	66.8	260	10	US-09-237-183A-2682
5	123.2	46.8	2218	18	US-10-437-963-65487
6	71.8	27.3	1577	17	US-10-424-599-3107
7	64.2	24.4	1482	17	US-10-282-122A-9984
8	61.8	23.5	1501	17	US-10-282-122A-9150
9	61.4	23.3	214	17	US-10-424-599-126220
10	61.4	23.3	1485	9	US-09-815-242-6958
11	61.4	23.3	1485	17	US-10-282-122A-22036

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14	61	23.2	1782	9	US-09-938-842A-2455	Sequence 2455, Ap	
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20	61	23.2	2632	18	US-10-425-115-162957	Sequence 162957, A	
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26	59	22.4	1731	11	US-09-938-842A-156	Sequence 156, App	
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29	58.2	22.1	1524	9	US-09-815-242-6547	Sequence 6547, Ap	
30	58.2	22.1	32768	9	US-09-070-927A-128	Sequence 128, App	
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36	55	20.9	2328	17	US-10-425-114-6121	Sequence 6121, Ap	
37	55	20.9	2812	17	US-10-424-599-31279	Sequence 31279, A	
38	54.6	20.8	2319	18	US-10-739-930-5533	Sequence 5533, Ap	
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43	52	19.8	1482	17	US-10-369-493-25835	Sequence 25835, A	
44	52	19.8	1524	17	US-10-282-122A-21509	Sequence 21509, A	
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ALIGNMENTS

RESULT 1
US-10-425-114-8171
; Sequence 8171, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8171
; LENGTH: 1680
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700737284_FLI
US-10-425-114-8171

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Best Local Similarity 89.4%; Score 235; DB 17; Length 1680;
Matches 238; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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DB 442 GAAGCATTGGATGGTTCGATGCTTCGACAGCAGTCTCAGACCCAGAGGATGG 501
QY 61 AATGCATTAATTTTGAAGAGCATTGGCTTTGATGACATTTCTCCATTAAGGTGACA 120

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Db 502 AATGCGATTAATTTGAGAGACCATTTGGCTTTGATGACCTTTCTCCCAAGGCTGACA 561.
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QY 181 AGGAATCNCAGTNAATAATCCCTNCAGGTTTAAAGGTTTCAANNANAGTTTGAAGCCACT 240
Db 622 AGGAATCTCATTTGAAAATCTTACAGTTTAAAGTTTCAATCTAGTTTGTGAGCCACTT 681
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Db 682 TGGAGTCGTACTTATATAGATPA 704
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RESULT 2
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/ Sequence 48573, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 48573
/ LENGTH: 2218
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_14868C.1
US-10-424-599-48573
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Query Match 89.4%; Score 235; DB 17; Length 2218;
Best Local Similarity 90.5%; Pred. No. 1.5e-59;
Matches 238; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY 1 GAAGCACTTTTGGATGTTGGCTGATGCTTTGCAAGACGCTGACAGCCAGAGGATGG 60
Db 894 GAAGCACTTTTGGATGTTGGCTGATGCTTTGCAAGACGCTGACAGCCAGAGGATGG 953
QY 61 AATCGCATTAATTTGAGAGCCATTTGGCTTTGATGACCTTTCCCATAGGCTGACA 120
Db 954 AATCGCATTAATTTGAGAGCCATTTGGCTTTGATGACCTTTCCCATAGGCTGACA 1013
QY 121 CAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGAAATTCATCTCTAGGA 180
Db 1014 CAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGAAATTCATCTCTAGGA 1073
QY 181 AGGAATCNCAGTNAATAATCCCTNCAGGTTTAAAGGTTTCAANNANAGTTTGAAGCCACT 240
Db 1074 AGGAATCTCATTTGAAAATCTTACAGTTTAAAGTTTCAATCTAGTTTGTGAGCCACTT 1133
QY 241 TNGAGNNAGNACTNNNNNANNA 263
Db 1134 TGGAGTCGTACTTATATAGATPA 1156
```

RESULT 3
US-09-237-183A-2682

```
/ Sequence 2682, Application US/09237183A
/ Publication No. US20030135870A1
/ GENERAL INFORMATION:
/ APPLICANT: Cheikh, No. US20030135870A1dine
/ APPLICANT: Fisher, Dane K.
/ APPLICANT: Liu, Jingsong
/ TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
```

```
/ TITLE OF INVENTION: Sucrose Pathway
/ FILE REFERENCE: 38-21(15089)B
/ CURRENT APPLICATION NUMBER: US/09/237,183A
/ CURRENT FILING DATE: 1999-01-26
/ PRIOR APPLICATION NUMBER: US 60/067,000
/ PRIOR FILING DATE: 1997-11-24
/ NUMBER OF SEQ ID NOS: 2814
/ SEQ ID NO 2682
/ LENGTH: 237
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(237)
/ OTHER INFORMATION: unsure at all n locations
US-09-237-183A-2682
```

Query Match 81.8%; Score 215.2; DB 10; Length 237;
Best Local Similarity 93.2%; Pred. No. 4e-54;
Matches 221; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY 1 GAAGCACTTTTGGATGTTGGCTGATGCTTTGCAAGACGCTGACAGCCAGAGGATGG 60
Db 1 GAAGCACTTTTGGATGTTGGCTGATGCTTTGCAAGACGCTGACAGCCAGAGGATGG 60
QY 61 AATCGCATTAATTTGAGAGCCATTTGGCTTTGATGACCTTTCCCATAGGCTGACA 120
Db 61 AATCGCATTAATTTGAGAGCCATTTGGCTTTGATGACCTTTCCCATAGGCTGACA 120
QY 121 CAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGAAATTCATCTCTAGGA 180
Db 121 CAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGAAATTCATCTCTAGGA 180
QY 181 AGGAATCNCAGTNAATAATCCCTNCAGGTTTAAAGGTTTCAANNANAGTTTGAAGCCA 237
Db 181 AGGAATCTCATTTGAAAATCTTACAGTTTAAAGGTTTCAAGCCAGATTTTGAAGCCA 237
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RESULT 4

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US-09-237-183A-2684
/ Sequence 2684, Application US/09237183A
/ Publication No. US20030135870A1
/ GENERAL INFORMATION:
/ APPLICANT: Cheikh, No. US20030135870A1dine
/ APPLICANT: Fisher, Dane K.
/ APPLICANT: Liu, Jingsong
/ TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
/ FILE REFERENCE: 38-21(15089)B
/ CURRENT APPLICATION NUMBER: US/09/237,183A
/ CURRENT FILING DATE: 1999-01-26
/ PRIOR APPLICATION NUMBER: US 60/067,000
/ PRIOR FILING DATE: 1997-11-24
/ NUMBER OF SEQ ID NOS: 2814
/ SEQ ID NO 2684
/ LENGTH: 260
/ TYPE: DNA
/ ORGANISM: Glycine max
US-09-237-183A-2684
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Query Match 66.8%; Score 175.8; DB 10; Length 260;
Best Local Similarity 87.0%; Pred. No. 2.6e-42;
Matches 180; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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QY 57 AATGATCGCATTAATTTGAGAGCCATTTGGCTTTGATGACCTTTCTCCCATAGGCT 116
Db 2 AATGATCGCATTAATTTGAGAGCCATTTGGCTTTGATGACCTTTCTCCCATAGGCT 61
QY 117 GACACAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGAAATTCATCTCTAGGA 176
Db 62 GACACAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGAAATTCATCTCTAGGA 121
QY 177 AGGAAGAAATCNCAGTNAATAATCCCTNCAGGTTTAAAGGTTTCAANNANAGTTTGAAGCC 236
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Db 122 AGGAAGATCTCATGAAATCTTACAGTTTAACTGTTTCAACTGTTTGAAGC 181
 Qy 237 ACCTTNGAGNNAGCTNNNNNANNA 263
 Db 182 ACTTGGAGTCTGACTTATATAGATTA 208

RESULT 5
 US-10-437-963-65487
 ; Sequence 65487, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbazuk, Brad
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 65487
 LENGTH: 2218
 TYPE: DNA
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_66530C.1
 US-10-437-963-65487

Query Match 46.8%; Score 123.2; DB 18; Length 2218;
 Best Local Similarity 66.0%; Pred. 4.1e-26;
 Matches 167; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 1 GAAGCATTGTTGATGTCGTCATGCTTTCAGAGCAGTCTCAGACCGAGAGGGATG 60
 Db 941 GAGGACCTTCTTGATGTTGACGTGACAGTGAAGGCCAACTATGAGAGGCTG 1000
 Qy 61 AATCGCATATTTTGAAGAGCCATTGGCTTTGATGACCTTTCCATAGGCTGACA 120
 Db 1001 AATAGGATATATGAGAGAACCATTTGGCTTCACCTGTTTCTTCAATCGGTTAACA 1060
 Qy 121 CAATATCTTCTTCAAACTTTCAGAGAAAGCAATATATGAAATGATGATCTACTAGGA 180
 Db 1061 CAATCATCTGCTGTCAGAGATTGAGGAGAGCATTTTACAGATGATCATCTTTTGAGG 1120
 Qy 181 AGGAATCAGTNAATAATCTTCAGGTTTAAAGGTTTCAANNAGTTTTCAGCCACT 240
 Db 1121 AAGGATCTGATGAAATCTCACCCGCTTGAAGATTTTCTAATTTGGTGTGACCTTTG 1180
 Qy 241 TNGAGNNAGCT 253
 Db 1181 TGAAGTCGACCT 1193

RESULT 6
 US-10-424-599-3107
 ; Sequence 3107, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 3107
 LENGTH: 1577
 TYPE: DNA
 ORGANISM: Glycine max
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(1577)
 OTHER INFORMATION: unsure at all n locations
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_102810C.1
 US-10-424-599-3107

Query Match 27.3%; Score 71.8; DB 17; Length 1577;
 Best Local Similarity 53.6%; Pred. No. 8.3e-11;
 Matches 133; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 6 ACTTTGATGTTGGTCACTGCTTGAAGCAGTGTCTGACCCAGAGAGGATGATG 65
 Db 716 ATTTGGATGTTGGAGATGCTGCTTAAGCTTCTTCAAAAGATGATGCAAG 775
 Qy 66 CATTAATTTTGAAGCCATTGGCTTGATGACCTTTCTTCCATAGGCTGACACATA 125
 Db 776 GGTATTTGTTGAAAAGCCATTGGTGTGATCTGACAGATCATTTAGTGAAGTAAAGAG 835
 Qy 126 TCTTCTTCAACTTTCAGAGAAAGCAATATATGATGATGATGATCTAAGAAAGAA 185
 Db 836 TTTGAAGCAGTACCTCAGAGAACCAATATATTCAGATGACATTTCTGGGTAAAGA 895
 Qy 186 TCCAGTNAATAATCTTCAGGTTTAAAGGTTTCAANNAGTTTTCAGCCACTTNGAG 245
 Db 896 GCTTGGAGATCTATGATGCTTCTTCAAAATCTTGTGAGCCCTGTGTGTC 955
 Qy 246 NNGNAGCT 253
 Db 956 CCGAAT 963

RESULT 7
 US-10-282-122A-9984
 ; Sequence 9984, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Foreyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625

;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9984
;; LENGTH: 1482
;; TYPE: DNA
;; ORGANISM: Bacillus anthracis
US-10-282-122A-9984

Query Match 24.4%; Score 64.2; DB 17; Length 1482;
Best Local Similarity 54.7%; Pred. No. 1.5e-08;
Matches 117; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 31 GCAAGCAGTGTCTGAGCCGGAAGGAGTGGATTCGATATTTTGAGAACCAATTTGGC 90
DB 400 GAAAGCGGACTGTATTAAGGATGATGAAAGCGCTAATGATGAAACCGTTGGG 459
QY 91 TTGTATGACCTTTCTTCCATAGGCTGACACAAATATCTTCAACTTTGAGAAAG 150
DB 460 CAGGACCTTACATCTGCTCGTAGCTGAATGATAGCTTAGCGACGTTTGAAGAGAC 519
QY 151 CAATATATATGATGTGATGATCTACTAGTGAAGATGATGATGATGATGATGATGAT 210
DB 520 GAGATATACCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 579
QY 211 AGGTTTCAANNAGTTTGTGAGCCACCTTNGA 244
DB 580 GAGTTTGCAAAATCTGTTTACATGATTTGCA 613

RESULT 8

US-10-282-122A-9150
; Sequence 9150, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931

;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9150
;; LENGTH: 1501
;; TYPE: DNA
;; ORGANISM: Bacillus anthracis
US-10-282-122A-9150

Query Match 23.5%; Score 61.8; DB 17; Length 1501;
Best Local Similarity 55.7%; Pred. No. 8e-08;
Matches 108; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 51 GAAGGATGGAATCGCATATATTTGAGAGCCATTTGGCTTTGATGACATTTCTTCCCA 110
DB 414 GATGGATGGAAGCGCTAATGATGAGAACCGTTGGGACGACCTTACATCTGCTG 473
QY 111 TAGGCTGACACATATCTTTCTTCAACTTTCAGGAAAGCAATATATAGATTGANCA 170
DB 474 TGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 533
QY 171 TCTACTAGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 230
DB 534 TTATTTAGGTAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 593
QY 231 TGAGCCACCTTNGA 244
DB 594 ACCATGATTTGGA 607

RESULT 9

US-10-424-599-126220
; Sequence 126220, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 126220
; LENGTH: 214
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(214)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_84985C.1
US-10-424-599-126220

Query Match 23.3%; Score 61.4; DB 17; Length 214;
Best Local Similarity 67.3%; Pred. No. 4e-08;
Matches 68; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 163 ATGATCATCTACTAGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 222
DB 1 ATGATCATCTACTAGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 223 NNAAGTTTGGAGCCACTTNGAGGAGGATGATGATGATGATGATGATGATGATGATGAT 263
DB 61 TTATTTTGGACCATGAAATCTCTTACATAGATAA 101

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RESULT 10
US-09-815-242-6958
; Sequence 6958, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6958
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1485)
US-09-815-242-6958

Query Match      23.3%; Score 61.4; DB 9; Length 1485;
Best Local Similarity 52.1%; Pred. No. 1e-07;
Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 53 AGGATGGAATGCAATATATTGAGAGCATTTGGCTTGATGCACTTTCCCAT 112
DB 422 ATGGCTGGAAGATATATCGTTGAAAACTTTTGTACGATGAAAAACAGCCCAA 481
QY 113 GGCTGACAAATATCTTCTTCAACTTCAGGAAAGCAATATATAGATGANCATC 172
DB 482 CATTAGACGTACAAATCCACCGTTCTTTGAGAAACCAAAATTATCGATGATCAT 541
QY 173 TACTAGGAAGATCNCAGTNAATAATCTCNCAGTTTAAAGGTTTCAANNAGNTTTG 232
DB 542 ATTTAGGTAAAGAAACCGTTCAAAACCTGCTGATTTAGGTTTCAAAATGTTGTTG 601
QY 233 AGCCACCTTNGAGNNGNACNTNNNNNANNA 263
DB 602 AACCGCTTGGAAACCGTAATTTCATTGATTA 632

RESULT 11
US-10-282-122A-22036
; Sequence 22036, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
```

```
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22036
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
US-10-282-122A-22036

Query Match      23.3%; Score 61.4; DB 17; Length 1485;
Best Local Similarity 52.1%; Pred. No. 1e-07;
Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 53 AGGATGGAATGCAATATATTGAGAGCATTTGGCTTGATGCACTTTCCCAT 112
DB 422 ATGGCTGGAAGATATATCGTTGAAAACTTTTGTACGATGAAAAACAGCCCAA 481
QY 113 GGCTGACAAATATCTTCTTCAACTTCAGGAAAGCAATATATAGATGANCATC 172
DB 482 CATTAGACGTACAAATCCACCGTTCTTTGAGAAACCAAAATTATCGATGATCAT 541
QY 173 TACTAGGAAGATCNCAGTNAATAATCTCNCAGTTTAAAGGTTTCAANNAGNTTTG 232
DB 542 ATTTAGGTAAAGAAACCGTTCAAAACCTGCTGATTTAGGTTTCAAAATGTTGTTG 601
QY 233 AGCCACCTTNGAGNNGNACNTNNNNNANNA 263
DB 602 AACCGCTTGGAAACCGTAATTTCATTGATTA 632

RESULT 12
US-10-329-670-1/C
; Sequence 1, Application US/10329670
; Publication No. US20040018503A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Sequence of the Haemophilus influenzae Rd Genome, Fragm
; FILE REFERENCE: PB186P1
```

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1  OTHER INFORMATION: n equals a, t, g or c
2  FEATURE:
3  NAME/KEY: misc_feature
4  LOCATION: (51602)..(51602)
5  OTHER INFORMATION: n equals a, t, g or c
6  FEATURE:
7  NAME/KEY: misc_feature
8  LOCATION: (51786)..(51786)
9  OTHER INFORMATION: n equals a, t, g or c
10 FEATURE:
11 NAME/KEY: misc_feature
12 LOCATION: (51805)..(51805)
13 OTHER INFORMATION: n equals a, t, g or c
14 FEATURE:
15 NAME/KEY: misc_feature
16 LOCATION: (55356)..(55356)
17 OTHER INFORMATION: n equals a, t, g or c
18 FEATURE:
19 NAME/KEY: misc_feature
20 LOCATION: (65309)..(65309)
21 OTHER INFORMATION: n equals a, t, g or c
22 FEATURE:
23 NAME/KEY: misc_feature
24 LOCATION: (65313)..(65313)
25 OTHER INFORMATION: n equals a, t, g or c
26 FEATURE:
27 NAME/KEY: misc_feature
28 LOCATION: (80024)..(80024)
29 OTHER INFORMATION: n equals a, t, g or c
30 FEATURE:
31 NAME/KEY: misc_feature
32 LOCATION: (100091)..(100091)
33 OTHER INFORMATION: n equals a, t, g or c
34 FEATURE:
35 NAME/KEY: misc_feature
36 LOCATION: (102596)..(102596)
37 OTHER INFORMATION: n equals a, t, g or c
38 FEATURE:
39 NAME/KEY: misc_feature
40 LOCATION: (105121)..(105121)
41 OTHER INFORMATION: n equals a, t, g or c
42 FEATURE:
43 NAME/KEY: misc_feature
44 LOCATION: (107248)..(107248)
45 OTHER INFORMATION: n equals a, t, g or c
46 FEATURE:
47 NAME/KEY: misc_feature
48 LOCATION: (117136)..(117136)
49 OTHER INFORMATION: n equals a, t, g or c
50 FEATURE:
51 NAME/KEY: misc_feature
52 LOCATION: (119750)..(119750)
53 OTHER INFORMATION: n equals a, t, g or c
54 FEATURE:
55 NAME/KEY: misc_feature
56 LOCATION: (119924)..(119924)
57 OTHER INFORMATION: n equals a, t, g or c
58 FEATURE:
59 NAME/KEY: misc_feature
60 LOCATION: (120038)..(120038)
61 OTHER INFORMATION: n equals a, t, g or c
62 FEATURE:
63 NAME/KEY: misc_feature
64 LOCATION: (121344)..(121344)
65 OTHER INFORMATION: n equals a, t, g or c
66 FEATURE:
67 NAME/KEY: misc_feature
68 LOCATION: (122167)..(122167)
69 OTHER INFORMATION: n equals a, t, g or c
70 FEATURE:
71 NAME/KEY: misc_feature
72 LOCATION: (122336)..(122336)
73 OTHER INFORMATION: n equals a, t, g or c

```



```

GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fragm
FILE REFERENCE: PB186P2CID1
CURRENT APPLICATION NUMBER: US/10/158,865
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1830121
TYPE: DNA
ORGANISM: Haemophilus influenzae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals a,t,c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals a,t,c, or g
FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,c, or g
FEATURE:
NAME/KEY: misc_feature

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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a,t,c, or g
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (122167)..(122167)

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OTHER INFORMATION: n equals a,t,c, or g
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals a,t,c, or g
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NAME/KEY: misc_feature
LOCATION: (152500)..(152500)
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NAME/KEY: misc_feature
LOCATION: (152530)..(152530)

Query Match 23.3%; Score 61.4; DB 18; Length 1830121;
Best Local Similarity 52.1%; Pred. No. 3.6e-06;
Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 53 AGGATGGATTCGATTAATTTTGAAGCATTTGGCTTTGATGACATTTCTCCATA 112
Db 577356 ATGGCTGGAACGTAATTAATGTTGAAAAACCTTTGGTTAGATGAAAAACAGCCAAA 577297
QY 113 GGCTGACACAATATCTCTTCAAACTTTCAGGAAAGCAAAATATATAGAAATGACATC 172
Db 577296 CATTAGACGTACAAATCCACCGTTTCTTTGAGAACACCAATTTATCGATGATCAT 577237
QY 173 TACTAGAGGAATTCACAGTNAATCTTCAGATTAAAGGTTTCAANNNAAGTTTG 232
Db 577236 ATTTAGTTAAAGAAACGTTCAAACTTCGTATTTAGCTTTTCAAAATGGTTGGTTG 577177
QY 233 AGCCACCTTGAGANNNAACNTNNNNGANNA 263
Db 577176 AACCGCTTGGAAACGTAATTCATTGATTA 577146

RESULT 14

US-09-938-842A-2455

Sequence 2455, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

FILE REFERENCE: SAME, AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/09/938,842A

PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 2455

LENGTH: 1782

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-2455

Query Match

Best Local Similarity 23.2%; Score 61; DB 9; Length 1782;

Matches 124; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Db

6 ACTTTGATGTTGGTCAATGCTTGCAGACAGTCTCAGACCCAGAGGATGATCG 65

675 ATTGTAGTCTGTGAAATGTGCAAGCACTTCTGCTCATGTCATGATGAGTAG 734

QY

66 CATTAATATTGAGAGCCATTGGCTTTGATGACATTTCCCATAGGCTGACACAATA 125

735 GGTATTCGTGCGAAGACCTTTGGTGTGAGATTCGAAACCTGGCTCTTTAAGCAATC 794

Db

126 TCTTCTTCAAACTTTCAGAAAGCAATATATAGATTTGATGATCTACTAGAGAGAA 185

795 CCTCAAGCAGTATTGGAGAGATCAATTTTGGATAGACATTAAGCAAGAGAA 854

QY

186 TNCAGTAAATCCTNCAGGTTTAAAGGTTTCAANNAGTTTGAAGCCACTTNG 243

855 GCTAGTCGAGAACTTATCTGTTCTTCGATTCCAACCTTATATTGAGCCGCTATGG 912

Db

US-09-938-842A-2455

Sequence 2455, Application US/09938842A

Patent No. US20040009476A9

ORGANISM: Arabidopsis thaliana

US-09-938-842A-2455

Query Match

Best Local Similarity 23.2%; Score 61; DB 11; Length 1782;

Matches 124; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Db

6 ACTTTGATGTTGGTCAATGCTTGCAGACAGTCTCAGACCCAGAGGATGATCG 65

675 ATTGTAGTCTGTGAAATGTGCAAGCACTTCTGCTCATGTCATGATGAGTAG 734

QY

66 CATTAATATTGAGAGCCATTGGCTTTGATGACATTTCCCATAGGCTGACACAATA 125

735 GGTATTCGTGCGAAGACCTTTGGTGTGAGATTCGAAACCTGGCTCTTTAAGCAATC 794

Db

126 TCTTCTTCAAACTTTCAGAAAGCAATATATAGATTTGATGATCTACTAGAGAGAA 185

795 CCTCAAGCAGTATTGGAGAGATCAATTTTGGATAGACATTAAGCAAGAGAA 854

QY

186 TNCAGTAAATCCTNCAGGTTTAAAGGTTTCAANNAGTTTGAAGCCACTTNG 243

855 GCTAGTCGAGAACTTATCTGTTCTTCGATTCCAACCTTATATTGAGCCGCTATGG 912

Db

Search completed: May 4, 2005, 21:11:33

Job time : 305.387 secs

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RESULT 2

US-09-313-294A-4756
; Sequence 4756, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Ito, Laura Y.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; NUMBER OF SEQ ID NOS: 1999-05-14
; SOFTWARE: PERL Program
; SEQ ID NO 4756
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700348987H1
; NAME/KEY: unsure
; LOCATION: 2, 72, 88
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4756

Query Match 39.3%; Score 161; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1,4e-34;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGGTATGGGGGAGAACTTGGCTTCAACATTGACAGAGAAAGGTTCCCATCTCTGTG 71
DB 106 GCGGTATGGGGGAGAACTTGGCTTCAACATTGACAGAGAAAGGTTCCCATCTCTGTG 165
QY 72 TACACAGAGACAACCTCCAGAGGACGAGACCGCTGACCGCCAGGACAGAGAAAC 131
DB 166 TACACAGAGACAACCTCCAGAGGACGAGACCGCTGACCGCCAGGACAGAGAAAC 225
QY 132 CTTCGGCTTACGGCTTCCATGACCCCGGCTCTTTGTGAA 172
DB 226 CTTCGGCTTACGGCTTCCATGACCCCGGCTCTTTGTGAA 266

RESULT 3

US-09-313-294A-6236
; Sequence 6236, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalagudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; NUMBER OF SEQ ID NOS: 1999-05-14
; SOFTWARE: PERL Program
; SEQ ID NO 6236
; LENGTH: 253
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700351460H1
US-09-313-294A-6236

Query Match 36.1%; Score 148; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 4,9e-31;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 GCGGTATGGGGGAGAACTTGGCTTCAACATTGACAGAGAAAGGTTCCCATCTCTGTG 71

DB 106 GCGGTATGGGGGAGAACTTGGCTTCAACATTGACAGAGAAAGGTTCCCATCTCTGTG 165
QY 72 TACACAGAGACAACCTCCAGAGGACGAGACCGCTGACCGCCAGGACAGAGAAAC 131
DB 166 TACACAGAGACAACCTCCAGAGGACGAGACCGCTGACCGCCAGGACAGAGAAAC 225
QY 132 CTTCGGCTTACGGCTTCCATGACCCCG 159
DB 226 CTTCGGCTTACGGCTTCCATGACCCCG 253

RESULT 4

US-09-902-540-4821
; Sequence 4821, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4821
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4821

Query Match 25.9%; Score 106.2; DB 4; Length 1404;
Best Local Similarity 56.3%; Pred. No. 2,3e-19;
Matches 223; Conservative 0; Mismatches 164; Indels 9; Gaps 1;

QY 15 GTCTATGGGGGAGAACTTGGCTTCAACATTGACAGAGAAAGGTTCCCATCTCTGTG 74
DB 25 GTCTATGGGGGAGAACTTGGCTTCAACATTGACAGAGAAAGGTTCCCATCTCTGTG 84
QY 75 AACAGAGACAACCTCCAGAGGACGAGACCGCTGACCGCCAGGACAGAGAAACCTT 134
DB 85 GAGAGC-----ATGCGAGCGCATGTGATGATGACCGCAACAGGACACCC 135
QY 135 CCGGTCTACGGCTTCCATGACCCCGCTCTTTGTGAAATCCATTGAGAGCGGATG 194
DB 136 GAGGTCTGGGGACCGAGTGTGAGAGCGCTTGTTCAGGACTGAGAGCGCCCGCAG 195
QY 195 GTGATCATGCTGTCAAGGCGCGCGCGCCAGTTGACCAACATCGCAGCTCGCAGCT 254
DB 196 GTGCTGTATGTGTGACGGCGCGCGCGCGGTGAGACTCATCTGAGCGCTGTGCGG 255
QY 255 CACTTGAAGAGGCGGACATGATCATGATGAGGAGGAGAGAGATGTAAGAGAGAG 314
DB 256 CTGATGGCGGAGAGCGGACGTCATCATGAGCGCGGCAATGCTGTGTCTGAGACGCGC 315
QY 315 AGGAGGAGAGAGCGCATGAGAGAGCGCGCTNCTGTATCTTGGCATGGGTCTTGTGA 374
DB 316 CGCCGCGAGAGAGAGTGCAGAGCGCAAGGCAATCTCTGTGGCGTGGCGCTGTCCGCG 375
QY 375 GGAAGAGAGGTGCGCGCAACGCGCTCTGTGATG 410
DB 376 GCGAGAGAGGCGCGCGCAACGCGCTCTCATCATG 411

RESULT 5

US-09-902-540-1237
; Sequence 1237, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-101(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1237
LENGTH: 26659
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-1237

Query Match 25.9%; Score 106.2; DB 4; Length 26659;
Best Local Similarity 56.3%; Pred. No. 6.5e-19;
Matches 223; Conservative 0; Mismatches 164; Indels 9; Gaps 1;

QY 15 GTCAATGGGGGAGAACTTGGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGTATC 74
DB 10955 GTCAATGGGGGAGAGCTTGCCTCAACATTCAGAGAAAGGTTCCCATCTCTGTATC 11014

QY 75 AACAGACAACTCCAGAGTGAAGAGACCGTGCAGCGTGCAGAGAGAGAAACCTT 134
DB 11015 GACAGGC-----ATCGAGAGCGCATTCATGATGATGACCGCAACAGAGACACCC 11065

QY 135 CCCGCTACAGGCTTCATGACCCCGCTCTTGTGAAGTCCATTCAGAGAGCAAGGAGT 194
DB 11066 GAGGCTCGGGGACCGAGTCCGTGAGGCGCTTCGTTAGCGAGTGAAGCGCCCGGCAAG 11125

QY 195 GTGATCATGCTCTCAAGAGCGCGCGCAAGTTGACCAACCATGCGACGTCGCACT 254
DB 11126 GTGCTGCTGATGATGACGCGCGCGCGGCTGAGCTCATGCTGAGACGCGCTGTCG 11185

QY 255 CACTTGAGAGAGGCGCATGATCATGATGAGGAGAAAGATGATGAGAGAGAGAG 314
DB 11186 CTGATGCGGAGAGAGGAGCTCATGATGAGAGCGCGCAACTGCTGCTTGGACAGCGCC 11245

QY 315 AGAGAGGAGAGAGGCGCATGAGAGAGCGCGCTCTGATGATGAGAGAGAGTCTCTGGA 374
DB 11246 CGCGCGGAGAGAGAGTGAAGAGCGCAAGGCAATCCATCTCGGGCGTGGCGTCCGCG 11305

QY 375 GGAAGAGAGGCTGCCCGCAAGCGCCGTCCTTGATG 410
DB 11306 GCGAGAGAGGCGCGCGCAAGCGCCCTTCATCATG 11341

RESULT 6
US-09-313-294A-5508
Sequence 5508, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalugudi, Raghunath V.
APPLICANT: Ito, Laura Y.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PI-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 5508
LENGTH: 294
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700350270H1
NAME/KEY: 51
LOCATION: 51
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-5508

Query Match 24.9%; Score 102; DB 4; Length 294;
Best Local Similarity 88.4%; Pred. No. 1.9e-18;
Matches 122; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 11 GCGGCTCATGGGAGAGAACTTGGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGT 70
DB 158 GCGGCTCATGGGAGAGAACTTGGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGT 217

QY 71 GTACACAGAGCAACTTCAGAGTGAAGAGACCGTGCAGCGTGCAGAGAGAGAA 130
DB 218 CTACACAGAGCAAA-CTTCAGAGTGAAGAGACCGTGCAGCGTGCAGAGAGAGAA 276

QY 131 CCTTCGCTTACGCGCTT 148
DB 277 CCTCCAGTGTGTGTTT 294

RESULT 7
US-09-103-840A-2/C
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 24.2%; Score 99.2; DB 3; Length 4403765;
Best Local Similarity 54.9%; Pred. No. 3.1e-16;
Matches 219; Conservative 0; Mismatches 174; Indels 6; Gaps 1;

QY 12 GCGGCTCATGGGAGAGAACTTGGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGT 71
DB 2092322 GCGGCTCATGGGAGAGAACTTGGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGT 2092263

QY 72 TACAACAGAGCAACTTCAGAGTGAAGAGACCGTGCAGCGTGCAGAGAGAGAAAC 131
DB 2092262 CACAATGCTGTGCTGCGCAAGACCGAGCGCTGTTAAGAGACAGCTGACAGGCAAG 2092203

QY 132 CTTCGCTTACAGGCTTCATGACCCGCGCTCTTGTGAAGTCCATTCAGAGCCAGG 191
DB 2092202 T-----TCGTGCGCAGTGAAGACATCCCGAATTTCTGCGGACATGGAAGAAACCGCGT 2092149

QY 192 GTGCTGATCATGCTGCTCAAGAGCGCGGCGGCGCAAGTTCAGAGACATTCGCAAGCTGCGCA 251
DB 2092148 CGGCTGCTGATCATGCTCAAGAGCGCGGAGAGCGCACTGATCATCAAGAACTTGTCT 2092089

QY 252 GCTCACTTGAAGAGAGGAGCATGATCATGATGAGGAGAGAGAGAGTGTGAGAGAGAG 311
DB 2092088 GAGCCATGAGAAACCGGAGCATATCATGAGAGCGGCAATGCTGTACAGCAAGCC 2092029

QY 312 GAGAGAGAGAGAGAGGCGCATGAGAGAGCGCGCTCTGATGATGATGATGATGATGATGATGAT 371
DB 2092028 ATGCGCGCGAGAGAGAGATGATGAGAGAGGCGCTTGAAGTGTGCGGCGCGGATATCC 2091969

QY 372 GAGAGAGAGAGAGGTTGCCCGCAAGCGCCGCTCTTGATG 410


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OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature

Query Match
Best Local Similarity 53.1%; Score 89.6; DB 4; Length 1230025;
Matches 213; Conservative 0; Mismatches 180; Indels 6; Gaps 1;

QY 12 GCGGTGATGGGAGAACCTTGCCCTCAATTCAGAGAAAGGTTCCCATCTGTG 71
DB 415812 GCTGTGATGGGAGAAATCTGTCTTAACATGATGATGATTTCTGTCTGTG 415753
QY 72 TACAACAGCAACCTCCAGGTGACGACCGGTGCAAGCGTCCAGAGCAAGAAAC 131
DB 415752 TATATCGAACCCCGAGAAAACCGGGACCTTTGAAAGATACCTTAACACCGAGAG 415693
QY 132 CTTCCGCTGACGGCTTCATGACCCCGGCTTTTGAGATGATTCATCAACAGCAGG 191
DB 415692 CTTGTAGGGTTGATCTTTTGA-----AGACTTTGAAATTCATTGAGACAGCA 415639
QY 192 GTGTGATCATGCTGTCAGAGCCGCGCCAGTTGACAGACCATCGACGCTGCA 251
DB 415638 AAGATCATGTTGATGATTCAGACAGGAAACCTGTGATCAGACATTCATGCTTACTG 415579
QY 252 GCTCATCTTGAGACAGGCGACTGCATCATGATGGGGAAACGAGTGTACGAGAACG 311
DB 415578 CTTTTCAGAACCCCGGAGTGTATTCATGATGGGGGATACCTATTTTAAAGATTCC 415519
QY 312 GAGAGAGGAGAAAGCCATGAGAGGCGCCCTGATCTTTGATGAGGCTGCT 371
DB 415518 GACGAGCATGTAAAGATTCAGAGAAAGGGATTTCTTTTTCAGGCTGGGGATTTCT 415459
QY 372 GAGGAAAGAGGGTGCCCGCAACGCGCCGCTTGTATG 410
DB 415458 GAGAGAGAAAGGTGACATGACGCGCCCATATATG 415420

RESULT 11
US-09-438-185A-1/c
Sequence 1, Application US/09438185A
Patent No. 682071
GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1230230
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-438-185A-1

Query Match
Best Local Similarity 53.1%; Score 88; DB 4; Length 1230230;
Matches 212; Conservative 0; Mismatches 181; Indels 6; Gaps 1;

QY 12 GCGGTGATGGGAGAACCTTGCCCTCAATTCAGAGAAAGGTTCCCATCTGTG 71
DB 405328 GCTGTGATGGGAGAAATCTGTCTTAACATGATGATGATTTCTGTCTGTG 405269
QY 72 TACAACAGCAACCTCCAGGTGACGACCGGTGCAAGCGTCCAGAGCAAGAAAC 131
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Db 405268 TATAATCGAGCCCGACAGAAAACGGGGGACTTCTTGAAGAATACCTTAACACCGGAGG 405209
 Qy 132 CTTCCTCCCTCTACGGCTTCCATGACCCCGGCTCTTTGGAAGTCCATTGACAGCCAGG 191
 Db 405208 CTGTGAGGGTTTGAATCTTTAGA-----AGATTTTGTGAATTCATTGAGAGACACAGA 405155
 Qy 192 GTGGGATCATGCTGCTGCAAGCGCGCGCGGCGGAGTGAACACAGATCGGACGCTCGCA 251
 Db 405154 AAGATCATGTTGATATTCACAGAGAAAACCTGTGATCAACAGCATTCATCGCTTACTG 405095
 Qy 252 GCTCATCTTGAGACAGGGGCACTGATCATTCATGAGGGGGAACAGATGTAGACAGAACG 311
 Db 405094 CCTTTTCTAGAACCCCGGGATGTGATTCATGAGGGGGAATAGCTATTTTAAAGATTCC 405035
 Qy 312 GAGAGAGAGAGAGAGCCATGAGAGAGCGCGCTTCTGATCTTGGCATGGGTTCTCT 371
 Db 405034 GAACGACCATGTAAAGATGTGAGAAAAGGGGATCTCTTCTTGAAGGGGAGATTCT 404975
 Qy 372 GGAGGAAAGAGAGGGTCCCGCAACGGCCGCTCTGATG 410
 Db 404974 GGAGGAGAGAGAGGTGACGTCACGCGCCCATCAATTATG 404936

RESULT 12

US-09-103-840A-1/c
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H3/RV
 ; US-09-103-840A-1

Query Match 20.9%; Score 85.8; DB 3; Length 4411529;
 Best Local Similarity 54.2%; Pred. No. 1.4e-12;
 Matches 218; Conservative 0; Mismatches 178; Indels 6; Gaps 2;

Qy 12 GCGGTCATGGGAGCAGAACCTTGCTCAACATGAGAGAAAAGGTTCCCATCTCTGTG 71
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 Qy 72 TACAAACAGACAACTCCAAAGTGAAGACAGACCGCTGACCGTCCCAAGGACAGAAAGAAC 131
 Db 2095072 CACATTCGCTGCTGCTGCAAGCCAGCGGCTGCTTAAGAGACCAAGCTCAACCGCAAG 2095013
 Qy 132 CTTCCTCCCTCTACGGCTTCCATGACCCCGGCTCTTTGTAAGTTCATTCAGAAAGCAGG 191
 Db 2095012 TT---CGTGGCAGTGAACAGATCCCGAATTTCTTCCGCACTGAAAAACCGGCTCG 2094956
 Qy 192 GTGGTATCATGCTC---GTCAAGCGCGCGGCGGCAAGTTGACCAATCGCGACGCTC 248
 Db 2094955 GTGGTATCATGCTCAAGCGCGGAGAGGCACTGACGCTGATGATCAACAACTT 2094896
 Qy 249 GCAGCTCATCTTGAGACAGGGGCACTGATCATTCATGAGGGGGAACAGATGTAGACAGAAC 308
 Db 2094895 GCTGACGCTATGAACCCGCGCAATCATCATGACGGGGGAATGCGTTGACACCGAC 2094836
 Qy 309 ACGGAGAGAGAGAGAGGCGCATGAGAGAGCGCGCTTCTGATCTTGGCATGGGTTGTC 368
 Db 2094835 ACCATGCGCGCGGAGAAAGCATGCTGAGCGGGGCTTGCACTTGTGCGGGCGCGGATC 2094776

Qy 369 TCTGAGAGAGAGAGGTCGCCGCAAGCGCCGCTCTTGATG 410
 Db 2094775 TCCGCGCGGAGAGAGGCGGCTTGAACGGCGCTGATCATG 2094734

RESULT 13

US-09-489-039A-1179
 ; Sequence 1179, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 1179
 ; LENGTH: 1473
 ; TYPE: DNA
 ; ORGANISM: Klebsiella pneumoniae
 ; US-09-489-039A-1179

Query Match 18.4%; Score 75.6; DB 4; Length 1473;
 Best Local Similarity 51.4%; Pred. No. 5.5e-11;
 Matches 205; Conservative 0; Mismatches 185; Indels 9; Gaps 1;

Qy 12 GCGGTCATGGGAGCAGAACCTTGCTCAACATGAGAGAAAAGGTTCCCATCTCTGTG 71
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 Qy 72 TACAAACAGACAACTCCAAAGTGAAGACAGACCGTGCAGCGTCCCAAGGACAGAAAGAAC 131
 Db 160 TTCAACCGCTCCCGGAAAGACGAGAAAGATGATGAGAGAAAACCGAGGACAGAACTG 219
 Qy 132 CTTCCTCCCTCTACGGCTTCCATGACCCCGGCTCTTTGTAAGTTCATTCAGAAAGCAGG 191
 Db 220 GTTCCTTATTAACAGATCAAGA-----ATTGTTAAATCCCTTGAACACACAGCT 270
 Qy 192 GTGGTATCATGCTGCTCAAGGCGCGCGCCAGTGAACAGACCATGCGGACGCTCGCA 251
 Db 271 GCTATCTGTTGATGCTGAAGCGCGGCTGCGACCGAGCGCATGACTCTCTGAAG 330
 Qy 252 GCTCATCTTGAGACAGGGGCACTGATCATTCATGAGGGGGAACAGATGTAGACAGAACAG 311
 Db 331 CTTTACCTTGATTAAGGCGACATCATCTTATGAGCGGCAACACTTCTTCAGAGACT 390
 Qy 391 ATCCGTGAAACCGGAGACTGCTGCGAAGGTTTAACTTATGATGATACCGGTGTTCC 450
 Qy 372 GGAGAAAGAGAGGTCGCCGCAAGCGCCGCTCTTGATG 410
 Db 451 GGTGTGAAGAGGGGCTGTGAAGGGCTTCCATCATG 489

RESULT 14

US-09-543-681A-1208
 ; Sequence 1208, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 1208
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1208

Query Match 16.1%; Score 66; DB 4; Length 1461;
Best Local Similarity 49.9%; Pred. No. 2.3e-08;
Matches 199; Conservative 0; Mismatches 191; Indels 9; Gaps 1;

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QY 12 GCGGTCATGGGGGAGAACCTTGGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGTG 71
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QY 72 TCAACAGAGCAACCTCCAGGTGACAGACCGTGCAGCGTCCCAAGCAGAGGAAC 131
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QY 132 CTTCCTGCTACGCGCTTCATGACCCCGGCTCTTTGTGAAGTCATTCAGAACCCAGG 191
DB 208 GTTCCGAAATTACTCTATTGAGA-----ATTGTTGATTTCATTAGAAAAACCGCT 258
QY 192 GTGGTATATGCTGCTCAAGCGCGCGCAATGACCAACATCGCAAGCTCGCA 251
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QY 252 GCTCACTTGAGAGAGGCGACTGCATCATGATGGGGGAGAGGTGTACGAGAACAG 311
DB 319 CCACATTTAGATTAAGGCGCATATCTTATTAAGGCGGAAATATCTTTTAAAGATACT 378
QY 312 GAGAGAGGAGAGAGCCATGAGAGCGCGCTNCTGATCTTATCTTGATGGTGTCTCT 371
DB 379 ATTCGTCGTAATCGTAGCTATCGGCTCAAGTTTAACTTATTTGATACGGGTCTTCT 438
QY 372 GAGAGAAAGAGGAGGCGCCGCAAGCGCCGCTTGATG 410
DB 439 GGTGTGAAGAGGCGCATTTAAAGAACCTTCTATTATG 477
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RESULT 15

US-09-710-279-1665
; Sequence 1665; Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1665
; LENGTH: 1407
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-1665

Query Match 15.3%; Score 62.8; DB 4; Length 1407;
Best Local Similarity 49.4%; Pred. No. 1.7e-07;
Matches 197; Conservative 0; Mismatches 193; Indels 9; Gaps 1;

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QY 72 TACAACAGACCAACCTCCAGAGTGAAGACCGTGCAGCGTCCCAAGGAGAGAAAC 131
DB 91 TATAACGATCAAGCAAAAACATGATGAATGTTAAAGATCGCTCGAAGAGAAATT 150
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QY 132 CTTCCTGCTACGCTTCATGACCCCGCGCTCTTTGTGAAGTCATTCCAGAACCCAGG 191
DB 151 TACCAACATTACTATTGAGA-----ATTGTAGATCTTTAGAGAACTCTGT 201
QY 192 GTGGTATCATGCTGCTCAAGCCCGCGCGCAGTGAACAGACCATCGCAGCGTGC 251
DB 202 AAGATTTTATTAATGTTAAAGCTGACCTGACACAGATGACCATTAATGATGTTATTA 261
QY 252 GCTCACTTGAGACAGGCGACTGCATCATGATGGGGGAAAGAGTGTACGAGAACAG 311
DB 262 CTTTATTAGACATGATGATATTTTATGATGTGTAATCTAATTTACCAAGATACG 321
QY 312 GAGAGAGGAGAAAGCCATGAGAGAGCGCGCTNCTGTAATCTTGATGAGTGTCTCT 371
DB 322 ATTCGTCGAAATTAAGCTTATGCTGAAGTATTAATTTATTTGATGAGGATTTCT 381
QY 372 GAGAGAAAGAGGAGGCGCCGCAAGCGCCGCTTGATG 410
DB 382 GGTGAGAAATCGGCGCACTCAGCGGCTTTCTTTAATG 420
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Job time : 137.974 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 465.167 Seconds
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Title: US-09-300-482-14

Perfect score: 410
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Searched: 5642217 seqs, 3043843248 residues

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Listing first 45 summaries

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Published Applications NA:*

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- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	396.4	96.7	748	US-10-425-115-91003	Sequence 91003, A
2	396.4	96.7	1587	US-10-425-114-6537	Sequence 6537, Ap
3	396.4	96.7	1624	US-10-425-114-30841	Sequence 30841, A
4	396.4	96.7	1661	US-10-425-114-24375	Sequence 24375, A
5	396.4	96.7	1669	US-10-425-114-15134	Sequence 31534, A
6	396.4	96.7	1671	US-10-425-114-1523	Sequence 1523, Ap
7	396.4	96.7	1672	US-10-425-114-24039	Sequence 24039, A
8	396.4	96.7	1672	US-10-425-114-32227	Sequence 32227, A
9	396.4	96.7	1674	US-10-425-114-13683	Sequence 13683, A
10	396.4	96.7	1675	US-10-425-114-446	Sequence 446, Ap
11	396.4	96.7	1691	US-10-425-114-28011	Sequence 28011, A

12	396.4	96.7	1781	US-10-425-114-3294	Sequence 3294, Ap
13	396.4	96.7	1798	US-10-425-114-508	Sequence 508, Ap
14	396.4	96.7	3520	US-10-425-115-91000	Sequence 91000, A
15	394.8	96.3	2171	US-10-425-114-2633	Sequence 2633, Ap
16	394.8	96.3	2469	US-10-425-115-91002	Sequence 91002, A
17	393.2	95.9	1650	US-10-425-114-3149	Sequence 3149, Ap
18	393.2	95.9	1678	US-10-425-114-4238	Sequence 4238, Ap
19	393.2	95.9	1678	US-10-425-114-3258	Sequence 13538, A
20	393.2	95.9	1678	US-10-425-114-24256	Sequence 24256, A
21	393.2	95.9	1678	US-10-425-114-25038	Sequence 25038, A
22	393.2	95.9	1681	US-10-425-114-4096	Sequence 4096, Ap
23	393.2	95.9	1684	US-10-425-114-25153	Sequence 25153, A
24	393.2	95.9	1686	US-10-425-114-3615	Sequence 3615, Ap
25	393.2	95.9	1728	US-10-425-114-4443	Sequence 4434, Ap
26	393.2	95.9	1740	US-10-425-114-24479	Sequence 24479, A
27	393.2	95.9	1798	US-10-425-114-1418	Sequence 1418, Ap
28	391.6	95.5	1872	US-10-425-114-26662	Sequence 26662, A
29	360	87.8	637	US-10-425-114-12436	Sequence 12436, A
30	360	87.8	637	US-10-425-115-91011	Sequence 91011, A
31	346.8	84.6	1953	US-10-767-701-14931	Sequence 14931, A
32	326	79.5	1831	US-10-437-963-98939	Sequence 98939, A
33	323.8	79.0	1755	US-10-425-114-32383	Sequence 32383, A
34	323.8	79.0	1776	US-10-425-114-3640	Sequence 3640, Ap
35	323.8	79.0	2343	US-10-425-115-127057	Sequence 127057, A
36	323.2	78.6	1125	US-10-425-115-44970	Sequence 44920, A
37	302.8	73.9	510	US-10-425-115-54519	Sequence 54519, A
38	262	63.9	1785	US-10-739-930-1129	Sequence 1129, Ap
39	242.8	59.2	1627	US-10-425-114-10641	Sequence 10641, A
40	242.8	59.2	1838	US-10-424-599-76904	Sequence 76904, A
41	234.8	57.3	4825	US-10-424-599-59918	Sequence 59918, A
42	231.6	56.5	1737	US-10-425-114-12849	Sequence 12849, A
43	230	56.1	2691	US-10-424-599-59924	Sequence 59924, A
44	215.8	52.6	286	US-09-294-093B-5229	Sequence 5229, Ap
45	207.6	50.6	901	US-10-424-599-66028	Sequence 66028, A

ALIGNMENTS

RESULT 1
US-10-425-115-91003
; Sequence 91003, Application US/10425115
; Publication NO. US2004021472NA1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 91003
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: M8T4577_182998C.1
; US-10-425-115-91003

Query Match 96.7%; Score 396.4; DB 18; Length 748;
Best Local Similarity 99.5%; Pred. No. 2.7e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGCGACAGACCTTGCTCCATTCGAGAGAAAGGTTCCCATCTCTGTG 71
DB 205 GCGGTCATGGGCGACAGACCTTGCTCCATTCGAGAGAAAGGTTCCCATCTCTGTG 264
QY 72 TACAACAGAGCAACCTCCAGAGGTGACGAGACCGTGACGCGTCCAGGACAGAGGAAC 131
DB 265 TACAACAGAGCAACCTCCAGAGGTGACGAGACCGTGACGCGTCCAGGACAGAGGAAC 324

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QY 132 CTTCCCGTCTAGGCTTCATGACCCCGCTCTTTGTGAAGTCCATTGAAAGCCACG 191
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Db 325 CTTCCCGTCTAGGCTTCATGACCCCGCTCTTTGTGAAGTCCATTGAAAGCCACG 384
QY 192 GTGGTATCATGCTCGTCAAGCGCGCGCCGCAATGACGACCATTCGAGCGCTGCA 251
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Db 385 GTGGTATCATGCTCGTCAAGCGCGCGCCGCAATGACGACCATTCGAGCGCTGCA 444
QY 252 GCTCACTTGAAGCGCGCGCACTGATCATGATGAGGGGAAACGAGTGTACGAAACAG 311
|
Db 445 GCTCACTTGAAGCGCGCGCACTGATCATGATGAGGGGAAACGAGTGTACGAAACAG 504
QY 312 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 371
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Db 505 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 564
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Db 565 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 603
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RESULT 2

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US-10-425-114-6537
; Sequence 6537, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6537
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700570587_FLI
US-10-425-114-6537
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Query Match 96.7%; Score 396.4; DB 17; Length 1587;
Best Local Similarity 99.5%; Pred. No. 36-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 72 TACAACAGAGCAACCTTCAAGGTGAGAGACCGGCGCGGCGCCCAAGCGAGAGAAAC 131
|
Db 93 TACAACAGAGCAACCTTCAAGGTGAGAGACCGGCGCGGCGCCCAAGCGAGAGAAAC 152
QY 132 CTTCCCGTCTAAGGCTTCCATGACCCCGCTCTTTGTGAAGTCCATTGAAAGCCACG 191
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Db 153 CTTCCCGTCTAAGGCTTCCATGACCCCGCTCTTTGTGAAGTCCATTGAAAGCCACG 212
QY 192 GTGGTATCATGCTCGTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 251
|
Db 213 GTGGTATCATGCTCGTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 272
QY 252 GCTCACTTGAAGCGCGCGCACTGATCATGATGAGGGGAAACGAGTGTACGAAACAG 311
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Db 273 GCTCACTTGAAGCGCGCGCACTGATCATGATGAGGGGAAACGAGTGTACGAAACAG 332
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Db 333 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 392
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; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 30841
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73088H07_FLI
US-10-425-114-30841
```

```
Query Match 96.7%; Score 396.4; DB 17; Length 1624;
Best Local Similarity 99.5%; Pred. No. 36-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 12 GGGTCATGAGGCGCAACCTTGCCTCAACATTTGAGAGAAAGGTTCCCATCTCTGTG 71
|
Db 70 GGGTCATGAGGCGCAACCTTGCCTCAACATTTGAGAGAAAGGTTCCCATCTCTGTG 129
QY 72 TACAACAGAGCAACCTTCAAGGTGAGAGACCGTGCAGCGGCGCCCAAGCGAGAGAAAC 131
|
Db 130 TACAACAGAGCAACCTTCAAGGTGAGAGACCGTGCAGCGGCGCCCAAGCGAGAGAAAC 189
QY 132 CTTCCCGTCTAAGGCTTCCATGACCCCGCTCTTTGTGAAGTCCATTGAAAGCCACG 191
|
Db 190 CTTCCCGTCTAAGGCTTCCATGACCCCGCTCTTTGTGAAGTCCATTGAAAGCCACG 249
QY 192 GTGGTATCATGCTCGTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 251
|
Db 250 GTGGTATCATGCTCGTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 309
QY 252 GCTCACTTGAAGCGCGCGCACTGATCATGATGAGGGGAAACGAGTGTACGAAACAG 311
|
Db 310 GCTCACTTGAAGCGCGCGCACTGATCATGATGAGGGGAAACGAGTGTACGAAACAG 369
QY 312 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 371
|
Db 370 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 429
QY 372 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 410
|
Db 430 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 468
```

RESULT 4

```
US-10-425-114-24375
; Sequence 24375, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
```

APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO: 24375
LENGTH: 1661
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3608-041-E4_FLI
US-10-425-114-24375

Query Match 96.7%; Score 396.4; DB 17; Length 1661;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGCGAGAGAAAGGTTCCCATCTCTGTG 71
DB 107 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGCGAGAGAAAGGTTCCCATCTCTGTG 166
QY 72 TACAACAGAGAACCTCCAGGTGAGACGACCGGTGCGAGCCGTCAGAGAGAGAAAC 131
DB 167 TACAACAGAGAACCTCCAGGTGAGACGACCGGTGCGAGCCGTCAGAGAGAGAAAC 226
QY 132 CTTCCTCGCTACGGCTTCCATGACCCCGGCTCTTGTGAAGTCCATTGAGAGAGAG 191
DB 227 CTTCCTCGCTACGGCTTCCATGACCCCGGCTCTTGTGAAGTCCATTGAGAGAGAG 286
QY 192 GTGGTATCATGCTCTGTCAGAGCGCGCGCCGAGTTGACAGACCATGCGAGCGTTCGA 251
DB 287 GTGGTATCATGCTCTGTCAGAGCGCGCGCCGAGTTGACAGACCATGCGAGCGTTCGA 346
QY 252 GCTCACTTGGAGAGAGGCGGATGATCATGATGGGGGAGAGAGTGTAGAGAGACAG 311
DB 347 GCTCACTTGGAGAGAGGCGGATGATCATGATGGGGGAGAGAGTGTAGAGAGACAG 406
QY 312 GAGAGAGAGAGAGGCGGATGAGAGAGCGCGCTTGTATCTTGGAGATGGGTCTCT 371
DB 407 GAGAGAGAGAGAGGCGGATGAGAGAGCGCGCTTGTATCTTGGAGATGGGTCTCT 466
QY 372 GAGAGAGAGAGAGGCGGATGAGAGAGCGCGCTTGTATCTTGGAGATGGGTCTCT 410
DB 467 GAGAGAGAGAGAGGCGGATGAGAGAGCGCGCTTGTATCTTGGAGATGGGTCTCT 505

RESULT 5
US-10-425-114-31534
Sequence 31534, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO: 31534
LENGTH: 1669
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73186B12_FLI

US-10-425-114-31534

Query Match 96.7%; Score 396.4; DB 17; Length 1669;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGCGAGAGAAAGGTTCCCATCTCTGTG 71
DB 115 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGCGAGAGAAAGGTTCCCATCTCTGTG 174
QY 72 TACAACAGAGAACCTCCAGGTGAGACGACCGGTGCGAGCCGTCAGAGAGAGAAAC 131
DB 175 TACAACAGAGAACCTCCAGGTGAGACGACCGGTGCGAGCCGTCAGAGAGAGAAAC 234
QY 132 CTTCCTCGCTACGGCTTCCATGACCCCGGCTCTTGTGAAGTCCATTGAGAGAGAG 191
DB 235 CTTCCTCGCTACGGCTTCCATGACCCCGGCTCTTGTGAAGTCCATTGAGAGAGAG 294
QY 192 GTGGTATCATGCTCTGTCAGAGCGCGCGCCGAGTTGACAGACCATGCGAGCGTTCGA 251
DB 295 GTGGTATCATGCTCTGTCAGAGCGCGCGCCGAGTTGACAGACCATGCGAGCGTTCGA 354
QY 252 GCTCACTTGGAGAGAGGCGGATGATCATGATGGGGGAGAGAGTGTAGAGAGACAG 311
DB 355 GCTCACTTGGAGAGAGGCGGATGATCATGATGGGGGAGAGAGTGTAGAGAGACAG 414
QY 312 GAGAGAGAGAGAGGCGGATGAGAGAGCGCGCTTGTATCTTGGAGATGGGTCTCT 371
DB 415 GAGAGAGAGAGAGGCGGATGAGAGAGCGCGCTTGTATCTTGGAGATGGGTCTCT 474
QY 372 GAGAGAGAGAGAGGCGGCGGAGAGCGCGCTTGTATCTTGGAGATGGGTCTCT 410
DB 475 GAGAGAGAGAGAGGCGGCGGAGAGCGCGCTTGTATCTTGGAGATGGGTCTCT 513

RESULT 6
US-10-425-114-1523
Sequence 1523, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO: 1523
LENGTH: 1671
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700156333_FLI
US-10-425-114-1523

Query Match 96.7%; Score 396.4; DB 17; Length 1671;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGCGAGAGAAAGGTTCCCATCTCTGTG 71
DB 117 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 176
QY 72 TACAACAGAGAACCTCCAGGTGAGACGACCGGTGCGAGCCGTCAGAGAGAGAAAC 131
DB 177 TACAACAGAGAACCTCCAGGTGAGACGACCGGTGCGAGCCGTCAGAGAGAGAAAC 236
QY 132 CTTCCTCGCTACGGCTTCCATGACCCCGGCTCTTGTGAAGTCCATTGAGAGAGAG 191

```
Db      237  |||||CTTCCCGCTACGCGTTTCATGATACCCCGCGCTCTTTGTGAAGTCCATTCAAAACCCACGG 296
Qy      192  GTGGTATCATGCTGCTGTCAAGCGCGCGCCAGTTGACAGACCATCGACGCTCGCA 251
Db      297  GTGGTATCATGCTGCTGTCAAGCGCGCGCCAGTTGACAGACCATCGACGCTCGCA 356
Qy      252  GCTCACTTGGAGGAGGCGGAGCTGATCATGATGAGGAGAAAGAGTGTACAGAACAG 311
Db      357  GCTCACTTGGAGGAGGCGGAGCTGATCATGATGAGGAGAAAGAGTGTACAGAACAG 416
Qy      312  GAGAGGAGGAGGAGGCGGAGCTGATCATGATGAGGAGGAGGAGGAGGAGGAGGAG 371
Db      417  GAGAGGAGGAGGAGGCGGAGCTGATCATGATGAGGAGGAGGAGGAGGAGGAGGAG 476
Qy      372  GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 410
Db      477  GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 515
```

RESULT 7

```
US-10-425-114-24039
; Sequence 24039, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With.
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 24039
; LENGTH: 1672
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB8607-006-H2_FLI
US-10-425-114-24039
```

```
Query Match      96.7%; Score 396.4; DB 17; Length 1672;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      12  GGGGTCAATGGGGCAAACTTGCCTCAACATTGCAAGAAAGGTTCCCATCTCTGTG 71
Db      118  GCGGTCAATGGGGCAAACTTGCCTCAACATTGCAAGAAAGGTTCCCATCTCTGTG 177
Qy      72  TACAACAGGACAACTCCCAAGGTGACGAGACCGGCGCCAGGCAAGGAGAAAC 131
Db      178  TACAACAGGACAACTCCCAAGGTGACGAGACCGGCGCCAGGCAAGGAGAAAC 237
Qy      132  CTTCCCGCTTACGCGCTTCCATGACCCCGCTCTTTGTGAAGTCCATTCAAAAGCCAG 191
Db      238  CTTCCCGCTTACGCGCTTCCATGACCCCGCTCTTTGTGAAGTCCATTCAAAAGCCAG 297
Qy      192  GTGGTATCATGCTGCTGTCAAGCGCGCGCGCATGTTGACGAGACCATCGACGCTCGCA 251
Db      298  GTGGTATCATGCTGCTGTCAAGCGCGCGCGCATGTTGACGAGACCATCGACGCTCGCA 357
Qy      252  GCTCACTTGGAGGAGGCGGAGCTGATCATGATGAGGAGGAGGAGGAGGAGGAGGAG 311
Db      358  GCTCACTTGGAGGAGGCGGAGCTGATCATGATGAGGAGGAGGAGGAGGAGGAGGAG 417
Qy      312  GAGAGGAGGAGGAGGCGGAGCTGATCATGATGAGGAGGAGGAGGAGGAGGAGGAG 371
Db      418  GAGAGGAGGAGGAGGCGGAGCTGATCATGATGAGGAGGAGGAGGAGGAGGAGGAG 477
```

```
Qy      372  GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 410
Db      478  GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 516
```

RESULT 8

```
US-10-425-114-32227
; Sequence 32227, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32227
; LENGTH: 1672
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73276H04_FLI
US-10-425-114-32227
```

```
Query Match      96.7%; Score 396.4; DB 17; Length 1672;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      12  GGGGTCAATGGGGCAAACTTGCCTCAACATTGCAAGAAAGGTTCCCATCTCTGTG 71
Db      118  GCGGTCAATGGGGCAAACTTGCCTCAACATTGCAAGAAAGGTTCCCATCTCTGTG 177
Qy      72  TACAACAGGACAACTCCCAAGGTGACGAGACCGGCGCCAGGCAAGGAGAAAC 131
Db      178  TACAACAGGACAACTCCCAAGGTGACGAGACCGGCGCCAGGCAAGGAGAAAC 237
Qy      132  CTTCCCGCTTACGCGCTTCCATGACCCCGCTCTTTGTGAAGTCCATTCAAAAGCCAG 191
Db      238  CTTCCCGCTTACGCGCTTCCATGACCCCGCTCTTTGTGAAGTCCATTCAAAAGCCAG 297
Qy      192  GTGGTATCATGCTGCTGTCAAGCGCGCGCGCATGTTGACGAGACCATCGACGCTCGCA 251
Db      298  GTGGTATCATGCTGCTGTCAAGCGCGCGCGCATGTTGACGAGACCATCGACGCTCGCA 357
Qy      252  GCTCACTTGGAGGAGGCGGAGCTGATCATGATGAGGAGGAGGAGGAGGAGGAGGAG 311
Db      358  GCTCACTTGGAGGAGGCGGAGCTGATCATGATGAGGAGGAGGAGGAGGAGGAGGAG 417
Qy      312  GAGAGGAGGAGGAGGCGGAGCTGATCATGATGAGGAGGAGGAGGAGGAGGAGGAG 371
Db      418  GAGAGGAGGAGGAGGCGGAGCTGATCATGATGAGGAGGAGGAGGAGGAGGAGGAG 477
Qy      372  GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 410
Db      478  GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 516
```

RESULT 9

```
US-10-425-114-13683
; Sequence 13683, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
```


APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 13683
LENGTH: 1674
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB143-023-B9_FLI
US-10-425-114-13683

Query Match 96.7%; Score 396.4; DB 17; Length 1674;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGCGAGAACCTTGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 71
DB 120 GCGGTCATGGGCGAGAACCTTGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 179
QY 72 TACAACAGAGCAACCTCCAGAGGTGAGACGACCGTGCAGCGTCCAGAGCAAGAAAC 131
DB 180 TACAACAGAGCAACCTCCAGAGGTGAGACGACCGTGCAGCGTCCAGAGCAAGAAAC 239
QY 132 CTTCCTGCTACGCGCTTCATGACCCCGCGCTCTTTGTAAGTTCATTGAGAGCAAGC 191
DB 240 CTTCCTGCTACGCGCTTCATGACCCCGCGCTCTTTGTAAGTTCATTGAGAGCAAGC 299
QY 192 GTGGTATCATGCTGTGTCAGAGCGCGCGCGCGAGTTGACCAACATGCGACGCTCGCA 251
DB 300 GTGGTATCATGCTGTGTCAGAGCGCGCGCGCGAGTTGACCAACATGCGACGCTCGCA 359
QY 252 GCTCACTTGAGACGAGCGCATGTCATTCATGAGGAGGAGAGAGTGTAGAGAAACAG 311
DB 360 GCTCACTTGAGACGAGCGCATGTCATTCATGAGGAGGAGAGTGTAGAGAAACAG 419
QY 312 GAGAGAGAGAGAGAGCGCATGAGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 371
DB 420 GAGAGAGAGAGAGAGCGCATGAGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 479
QY 372 GAGAGAGAGAGAGAGCGCGCATGAGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 410
DB 480 GAGAGAGAGAGAGAGCGCGCATGAGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 518

RESULT 10

US-10-425-114-446
Sequence 446, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 446
LENGTH: 1675
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700075354_FLI
US-10-425-114-446

Query Match 96.7%; Score 396.4; DB 17; Length 1675;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGCGAGAACCTTGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 71
DB 121 GCGGTCATGGGCGAGAACCTTGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 180
QY 72 TACAACAGAGCAACCTCCAGAGGTGAGACGACCGTGCAGCGTCCAGAGCAAGAAAC 131
DB 181 TACAACAGAGCAACCTCCAGAGGTGAGACGACCGTGCAGCGTCCAGAGCAAGAAAC 240
QY 132 CTTCCTGCTACGCGCTTCATGACCCCGCGCTCTTTGTAAGTTCATTGAGAGCAAGC 191
DB 241 CTTCCTGCTACGCGCTTCATGACCCCGCGCTCTTTGTAAGTTCATTGAGAGCAAGC 300
QY 192 GTGGTATCATGCTGTGTCAGAGCGCGCGCGCGAGTTGACCAACATGCGACGCTCGCA 251
DB 301 GTGGTATCATGCTGTGTCAGAGCGCGCGCGCGAGTTGACCAACATGCGACGCTCGCA 360
QY 252 GCTCACTTGAGACGAGCGCATGTCATTCATGAGGAGGAGAGAGTGTAGAGAAACAG 311
DB 361 GCTCACTTGAGACGAGCGCATGTCATTCATGAGGAGGAGAGAGTGTAGAGAAACAG 420
QY 312 GAGAGAGAGAGAGAGCGCATGAGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 371
DB 421 GAGAGAGAGAGAGAGCGCATGAGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 480
QY 372 GAGAGAGAGAGAGAGCGCGCATGAGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 410
DB 481 GAGAGAGAGAGAGAGCGCGCATGAGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 519

RESULT 11

US-10-425-114-28011
Sequence 28011, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28011
LENGTH: 1691
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4743-047-F5_FLI
US-10-425-114-28011

Query Match 96.7%; Score 396.4; DB 17; Length 1691;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGCGAGAACCTTGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 71
DB 134 GCGGTCATGGGCGAGAACCTTGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 193
QY 72 TACAACAGAGCAACCTCCAGAGGTGAGACGACCGTGCAGCGTCCAGAGCAAGAAAC 131
DB 194 TACAACAGAGCAACCTCCAGAGGTGAGACGACCGTGCAGCGTCCAGAGCAAGAAAC 253
QY 132 CTTCCTGCTACGCGCTTCATGACCCCGCGCTCTTTGTAAGTTCATTGAGAGCAAGC 191
DB 254 CTTCCTGCTACGCGCTTCATGACCCCGCGCTCTTTGTAAGTTCATTGAGAGCAAGC 313

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QY 192 GTGTGATCATGCTGTCAGAGCGCGCGCCACTTGATCCAGACATCGGAGCGCTCGCA 251
|
Db 314 GTGTGATCATGCTGTCAGAGCGCGCGCCACTTGATCCAGACATCGGAGCGCTCGCA 373
QY 252 GCTCACTTGGAGCAGGCGCACTGCATCATGATGGGGGAAAGAGTGTGTAAGAAACAG 311
|
Db 374 GCTCACTTGGAGCAGGCGCACTGCATCATGATGGGGGAAAGAGTGTGTAAGAAACAG 433
QY 312 GAGAGGAGGAGAAAGGCGCATGAGAGACCGCGCTTCTGATCTTGGCATGGGTCTCT 371
|
Db 434 GAGAGGAGGAGAAAGGCGCATGAGAGACCGCGCTTCTGATCTTGGCATGGGTCTCT 493
QY 372 GAGAGAAAGAGGAGGCGCGCCCAACGCGCGCTCTTGATG 410
|
Db 494 GAGAGAGAGAGGAGGCGCGCCCAACGCGCGCTCTTGATG 532

RESULT 12
US-10-425-114-3294
; Sequence 3294, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3294
; LENGTH: 1781
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700258317_FLI
US-10-425-114-3294

Query Match          96.7%; Score 396.4; DB 17; Length 1781;
Best Local Similarity 99.5%; Pred. No. 3.1e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGCGAGAACTTGCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 71
|
Db 227 GCGGTCATGGGCGAGAACTTGCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 286
QY 72 TACAACAGAGCAACTCCAGGTGAGAGAGACCGTGCAGCGTCCCAAGAGCAAGAAAC 131
|
Db 287 TACAACAGAGCAACTCCAGGTGAGAGAGACCGTGCAGCGTCCCAAGAGCAAGAAAC 346
QY 132 CTTCCGCTTAAGCGCTTCAATGACCCCGGCTCTTGGAGTGCATTCAAGACACAGG 191
|
Db 347 CTTCCGCTTAAGCGCTTCAATGACCCCGGCTCTTGGAGTGCATTCAAGACACAGG 406
QY 192 GTGTGATCATGCTGTCAGAGCGCGCGCGCATGTAACAGACCATGCGACCTCGCA 251
|
Db 407 GTGTGATCATGCTGTCAGAGCGCGCGCGCATGTAACAGACCATGCGACCTCGCA 466
QY 252 GCTCACTTGGAGCAGGCGCACTGCATCATGATGGGGGAAAGAGTGTGTAAGAAACAG 311
|
Db 467 GCTCACTTGGAGCAGGCGCACTGCATCATGATGGGGGAAAGAGTGTGTAAGAAACAG 526
QY 312 GAGAGGAGGAGAAAGGCGCATGAGAGCGCGCTTCTGATCTTGGCATGGGTCTCT 371
|
Db 527 GAGAGGAGGAGAAAGGCGCATGAGAGCGCGCTTCTGATCTTGGCATGGGTCTCT 586
QY 372 GAGAGAAAGAGGAGGCGCGCCCAACGCGCGCTCTTGATG 410
|
|
|
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```
Db 587 GAGAGAGAGAGGAGGCGCGCCCAACGCGCGCTCTTGATG 625

RESULT 13
US-10-425-114-508
; Sequence 508, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 508
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700076402_FLI
US-10-425-114-508

Query Match          96.7%; Score 396.4; DB 17; Length 1798;
Best Local Similarity 99.5%; Pred. No. 3.1e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGCGAGAACTTGCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 71
|
Db 120 GCGGTCATGGGCGAGAACTTGCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 179
QY 72 TACAACAGAGCAACTCCAGGTGAGAGAGACCGTGCAGCGTCCCAAGAGCAAGAAAC 131
|
Db 180 TACAACAGAGCAACTCCAGGTGAGAGAGACCGTGCAGCGTCCCAAGAGCAAGAAAC 239
QY 132 CTTCCGCTTAAGCGCTTCAATGACCCCGGCTCTTGGAGTGCATTCAAGACACAGG 191
|
Db 240 CTTCCGCTTAAGCGCTTCAATGACCCCGGCTCTTGGAGTGCATTCAAGACACAGG 239
QY 192 GTGTGATCATGCTGTCAGAGCGCGCGCGCATGTAACAGACCATGCGACCTCGCA 251
|
Db 300 GTGTGATCATGCTGTCAGAGCGCGCGCGCATGTAACAGACCATGCGACCTCGCA 359
QY 252 GCTCACTTGGAGCAGGCGCACTGCATCATGATGGGGGAAAGAGTGTGTAAGAAACAG 311
|
Db 360 GCTCACTTGGAGCAGGCGCACTGCATCATGATGGGGGAAAGAGTGTGTAAGAAACAG 419
QY 312 GAGAGGAGGAGAAAGGCGCATGAGAGCGCGCTTCTGATCTTGGCATGGGTCTCT 371
|
Db 420 GAGAGGAGGAGAAAGGCGCATGAGAGCGCGCTTCTGATCTTGGCATGGGTCTCT 479
QY 372 GAGAGAAAGAGGAGGCGCGCCCAACGCGCGCTCTTGATG 410
|
Db 480 GAGAGAGAGAGGAGGCGCGCCCAACGCGCGCTCTTGATG 518

RESULT 14
US-10-425-115-91000
; Sequence 91000, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
```

CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 91000
LENGTH: 3520
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_182995C.1
US-10-425-115-91000

Query Match 96.7%; Score 396.4; DB 18; Length 3520;
Best Local Similarity 99.5%; Pred. No. 3.4e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCAATGAGGAGCAACCTTCCCTCAACATTGACAGAAAGGGTTCCCATCTCTGTG 71
DB 1319 GCGGTCAATGAGGAGCAACCTTCCCTCAACATTGACAGAAAGGGTTCCCATCTCTGTG 1378
QY 72 TACAACAGGACAACCTCCCAAGGTGACGACCGTGCAGCGCCAGGCAAGGCAAGAAAC 131
DB 1379 TACAACAGGACAACCTCCCAAGGTGACGACCGTGCAGCGCCAGGCAAGGCAAGAAAC 1438
QY 132 CTTCCTGCTACGCGCTTCCATGACCCCGCGTCTTTGTAAGTCCATTGAGCAAGCCAG 191
DB 1439 CTTCCTGCTACGCGCTTCCATGACCCCGCGTCTTTGTAAGTCCATTGAGCAAGCCAG 1498
QY 192 GTGTGATCATGCTGTGTCAGAGCGCGCGCCGACGTTGACCAACCATGCGACGCTGCA 251
DB 1499 GTGTGATCATGCTGTGTCAGAGCGCGCGCCGACGTTGACCAACCATGCGACGCTGCA 1558
QY 252 GCTCACTTGGAGCAGGCGCATGTCATTCGATGGGGGGAAGAGTGTACAGAAACAG 311
DB 1559 GCTCACTTGGAGCAGGCGCATGTCATTCGATGGGGGGAAGAGTGTACAGAAACAG 1618
QY 312 GAGAGGAGGAGAAAGCCATGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 371
DB 1619 GAGAGGAGGAGAAAGCCATGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 1678
QY 372 GAGGAAAGAGAGGGTCCCGCAAGCGCCGCTCTTGATG 410
DB 1679 GAGGAGAGAGAGGGTCCCGCAAGCGCCGCTCTTGATG 1717

RESULT 15

US-10-425-114-2633
Sequence 2633, Application US/10425114
Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 2633
LENGTH: 2171
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700219903_FLI
US-10-425-114-2633

Query Match 96.3%; Score 394.8; DB 17; Length 2171;
Best Local Similarity 99.2%; Pred. No. 1e-112;
Matches 396; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 GCGGTCAATGAGGAGCAACCTTCCCTCAACATTGACAGAAAGGGTTCCCATCTCTGTG 71
DB 617 GCGGTCAATGAGGAGCAACCTTCCCTCAACATTGACAGAAAGGGTTCCCATCTCTGTG 676
QY 72 TACAACAGGACAACCTCCCAAGGTGACGACCGTGCAGCGCCAGGCAAGGCAAGAAAC 131
DB 677 TACAACAGGACAACCTCCCAAGGTGACGACCGTGCAGCGCCAGGCAAGGCAAGAAAC 736
QY 132 CTTCCTGCTACGCGCTTCCATGACCCCGCGTCTTTGTAAGTCCATTGAGCAAGCCAG 191
DB 737 CTTCCTGCTACGCGCTTCCATGACCCCGCGTCTTTGTAAGTCCATTGAGCAAGCCAG 796
QY 192 GTGTGATCATGCTGTGTCAGAGCGCGCGCCGACGTTGACCAACCATGCGACGCTGCA 251
DB 797 GTGTGATCATGCTGTGTCAGAGCGCGCGCCGACGTTGACCAACCATGCGACGCTGCA 856
QY 252 GCTCACTTGGAGCAGGCGCATGTCATTCGATGGGGGGAAGAGTGTACAGAAACAG 311
DB 857 GCTCACTTGGAGCAGGCGCATGTCATTCGATGGGGGGAAGAGTGTACAGAAACAG 916
QY 312 GAGAGGAGGAGAAAGCCATGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 371
DB 917 GAGAGGAGGAGAAAGCCATGAGAGCGCGCTCTGATCTTGGCATGGGTGTCTCT 976
QY 372 GAGGAAAGAGAGGGTCCCGCAAGCGCCGCTCTTGATG 410
DB 977 GAGGAGAGAGAGGGTCCCGCAAGCGCCGCTCTTGATG 1015

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Job time : 467.167 secs

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 68.1803 Seconds
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Title: US-09-300-482-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49.6	21.3	744	US-09-248-796A-3185	Sequence 3185, App
2	34.6	14.8	507	US-09-134-001C-2798	Sequence 2798, App
3	34.6	14.8	597	US-09-710-279-185	Sequence 185, App
4	34.6	14.8	2845	US-09-710-279-3371	Sequence 3371, App
5	34.6	14.8	3825	US-09-710-279-3794	Sequence 3794, App
6	31.6	13.6	84296	US-09-949-016-17375	Sequence 17375, A
7	31.2	13.4	4358	US-08-956-171E-454	Sequence 454, App
8	31.2	13.4	4358	US-08-781-986A-454	Sequence 454, App
9	30.8	13.2	601	US-09-949-016-65898	Sequence 65898, A
10	30.6	13.1	92139	US-09-918-686-1	Sequence 1, App1
11	30.6	13.1	390416	US-09-949-016-16923	Sequence 16923, A
12	30.2	13.0	601	US-09-949-016-168377	Sequence 168377, A
13	30.2	13.0	14449	US-09-949-016-12108	Sequence 12108, A
14	30.2	13.0	29628	US-09-949-016-16483	Sequence 16483, A
15	30	12.9	63385	US-09-949-016-14856	Sequence 14856, A
16	29.8	12.8	5280	US-08-956-171E-544	Sequence 544, App
17	29.8	12.8	5280	US-08-781-986A-544	Sequence 544, App
18	29.8	12.8	7655	US-08-619-554-1	Sequence 1, App1
19	29.6	12.7	65042	US-09-784-316-3	Sequence 3, App1
20	29.6	12.7	65042	US-10-229-124-3	Sequence 3, App1
21	29.6	12.7	235452	US-09-949-016-13675	Sequence 13675, A
22	29.4	12.6	466	US-09-270-767-28500	Sequence 28500, A
23	29.4	12.6	601	US-09-949-016-24050	Sequence 24050, A
24	29.4	12.6	601	US-09-949-016-53690	Sequence 53690, A
25	29.4	12.6	601	US-09-949-016-197767	Sequence 197767, A
26	29.4	12.6	1170	US-09-248-796A-618	Sequence 618, App
27	29.4	12.6	1506	US-09-540-236-158	Sequence 158, App

C	28	29.4	12.6	1533	4	US-09-270-767-12691	Sequence 12691, A
C	29	29.4	12.6	14335	4	US-09-596-002-11	Sequence 11, App1
C	30	29.4	12.6	24405	4	US-09-949-016-12040	Sequence 12040, A
C	31	29.4	12.6	24405	4	US-09-949-016-17346	Sequence 17346, A
C	32	29.4	12.6	250715	4	US-09-949-016-13294	Sequence 13294, A
C	33	29.4	12.6	393753	4	US-09-949-016-14573	Sequence 14573, A
C	34	29.4	12.6	393753	4	US-09-949-016-14574	Sequence 14574, A
C	35	29.4	12.6	818128	4	US-09-949-016-14546	Sequence 14546, A
C	36	29.4	12.6	818128	4	US-09-949-016-14547	Sequence 14547, A
C	37	29.4	12.6	818128	4	US-09-949-016-14548	Sequence 14548, A
C	38	29.4	12.6	818128	4	US-09-949-016-14549	Sequence 14549, A
C	39	29.4	12.6	818128	4	US-09-949-016-14550	Sequence 14550, A
C	40	29.4	12.6	818128	4	US-09-949-016-14551	Sequence 14551, A
C	41	29.4	12.6	818128	4	US-09-949-016-14552	Sequence 14552, A
C	42	29.4	12.6	818128	4	US-09-949-016-14553	Sequence 14553, A
C	43	29.4	12.6	818128	4	US-09-949-016-14554	Sequence 14554, A
C	44	29.4	12.6	818128	4	US-09-949-016-14555	Sequence 14555, A
C	45	29.4	12.6	818128	4	US-09-949-016-14556	Sequence 14556, A

ALIGNMENTS

```
RESULT 1
US-09-248-796A-3185
; Sequence 3185, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 3185
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Candida albicans
; US-09-248-796A-3185

Query Match
Best Local Similarity 53.8%; Pred. No. 8.9e-07;
Matches 128; Conservative 0; Mismatches 104; Indels 6; Gaps 1;

QY 2 TTTTTCAGTTAGTGAATATGCTTCTCTATGATGAGGTGGAAGATTGAGTTA 61
DB 262 TTTTAAAACTGTTTCATATATTTGTGACCTTATGATGATGAGTGAAGATTAAAAA 321
QY 62 TTGAATGAGGCAATCTCGATGATGA-----GACTGAGAAAAAATGACTCGGGAAC 115
DB 322 TTGAATGAGGCAATCTCGATGATGA-----GACTGAGAAAAAATGATGATGATGAT 381
QY 116 TACCCAGATATTTTATTTTGGCATTCGCTTCATGATCCATCGATGATGCGAGATG 175
DB 382 CCCGAAAGTATTTTATTTTGGCATTCACCATGATGATGATGATGATGATGATGAT 441
QY 176 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 233
DB 442 GTTAAAAAAATGTTTATTCACACGAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 499

RESULT 2
US-09-134-001C-2798
; Sequence 2798, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
```

/ TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: GTC-007
/ CURRENT APPLICATION NUMBER: US/09/134,001C
/ CURRENT FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/064,964
/ PRIOR FILING DATE: 1997-11-08
/ PRIOR APPLICATION NUMBER: US 60/055,779
/ PRIOR FILING DATE: 1997-08-14
/ NUMBER OF SEQ ID NOS: 5674
/ SEQ ID NO 2798
/ LENGTH: 507
/ TYPE: DNA
/ ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2798

Query Match 14.8%; Score 34.6; DB 3; Length 507;
Best Local Similarity 61.8%; Pred. No. 0.095;
Matches 55; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 11 TTACTAGAAATATGTTAGTGGCTCCTATGATAGGATGAGGATTTGAGTTATGAAATGAG 70
DB 310 TTAGAAGATTATTAATTAATGACGAGAGATTAATGCGCAATTATTAATGTAATCA 369

QY 71 GCAATCTCTGAGTATGAGACTTCAGAAA 99
DB 370 CTAACTCTGATTATCAAAACCCAGAGA 398

RESULT 3
US-09-710-279-185
/ Sequence 185, Application US/09/10279
/ Patent No. 6703492
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: P03480US
/ CURRENT APPLICATION NUMBER: US/09/710,279
/ CURRENT FILING DATE: 2000-11-09
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 185
/ LENGTH: 597
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: nucleic acid sequence
US-09-710-279-185

Query Match 14.8%; Score 34.6; DB 4; Length 597;
Best Local Similarity 61.8%; Pred. No. 0.1;
Matches 55; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 11 TTAGTGAATATGTTAGTGGCTCCTATGATAGGATGAGGATTTGAGTTATGAAATGAG 70
DB 436 TTAGAAGATTATTAATTAATGACGAGAGTACTGGCAATTATTAATGTAATCA 495

QY 71 GCAATCTCTGAGTATGAGACTTCAGAAA 99
DB 496 CTAACTCTGATTATCAAAACCCAGAGA 524

RESULT 4
US-09-710-279-3371/c
/ Sequence 3371, Application US/09/10279
/ Patent No. 6703492
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: P03480US
/ CURRENT APPLICATION NUMBER: US/09/710,279

/ CURRENT FILING DATE: 2000-11-09
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3371
/ LENGTH: 2945
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3371

Query Match 14.8%; Score 34.6; DB 4; Length 2945;
Best Local Similarity 61.8%; Pred. No. 0.21;
Matches 55; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 11 TTAGTGAATATGTTAGTGGCTCCTATGATAGGATGAGGATTTGAGTTATGAAATGAG 70
DB 162 TTAGAAGATTATTAATTAATGACGAGAGATTAATGCGCAATTATTAATGTAATCA 103

QY 71 GCAATCTCTGAGTATGAGACTTCAGAAA 99
DB 102 CTAACTCTGATTATCAAAACCCAGAGA 74

RESULT 5
US-09-710-279-3794/c
/ Sequence 3794, Application US/09/10279
/ Patent No. 6703492
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: P03480US
/ CURRENT APPLICATION NUMBER: US/09/710,279
/ CURRENT FILING DATE: 2000-11-09
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3794
/ LENGTH: 3825
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3794

Query Match 14.8%; Score 34.6; DB 4; Length 3825;
Best Local Similarity 61.8%; Pred. No. 0.24;
Matches 55; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 11 TTAGTGAATATGTTAGTGGCTCCTATGATAGGATGAGGATTTGAGTTATGAAATGAG 70
DB 780 TTAGAAGATTATTAATTAATGACGAGAGTACTGGCAATTATTAATGTAATCA 721

QY 71 GCAATCTCTGAGTATGAGACTTCAGAAA 99
DB 720 CTAACTCTGATTATCAAAACCCAGAGA 692

RESULT 6
US-09-949-016-17375/c
/ Sequence 17375, Application US/09/949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: C0001307
/ CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 17375
LENGTH: 84296
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(84296)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17375

Query Match 13.6%; Score 31.6; DB 4; Length 84296;
Best Local Similarity 51.4%; Pred. No. 10;
Matches 73; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 52 ATTGAGTATTGATGAGGACATCTCGATGATGAGACTTCAGAAACATGACTCGGG 111
DB 70175 ATTGGGTCATTGGTTAGACATGTTGCCAGGCTTCCACTATACATGACTCTTT 70116
QY 112 AAGCTACCGCAGATTATTTATTGGCATTCCTCCATCAGTCTACCCATCAGTATGCA 171
DB 70115 CACCTTGCATATCTGTTCTTTGGAAGTACTAAATCCAGCTGTACTTAAGG 70056
QY 172 GATGATAGATCATATTCATG 193
DB 70055 GAGAAATAGTATATCTCCCTG 70034

RESULT 7
US-08-956-171E-454
Sequence 454, Application US/08956171E.
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 454:
SEQUENCE CHARACTERISTICS:
LENGTH: 4358 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 454:
US-08-956-171E-454

Query Match 13.4%; Score 31.2; DB 4; Length 4358;
Best Local Similarity 53.2%; Pred. No. 3.6;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 48 AAGATTGATTGATGAGGACATCTCGATGATGAGACTTCAGAAACATGACT 107
DB 1252 AAGATTGATTGATTGATGAGGACATCTCGATGATGAGACTTCAGAAACATGACT 1311
QY 108 CGGAGCTACCGCAGATTATTTATTGGCATTCCTCCATCAGTCTACCCATCAGTAT 167
DB 1312 TGGTTAAGTATCATATTTATTGTTTGAAGCAGCAGCAATTAATATGAT 1371
QY 168 GCGA 171
DB 1372 CCTA 1375

RESULT 8
US-08-781-986A-454
Sequence 454, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 454:
SEQUENCE CHARACTERISTICS:
LENGTH: 4358 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-454

Query Match 13.4%; Score 31.2; DB 4; Length 4358;

Best Local Similarity 53.2%; Pred. No. 3.6;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 48 AAGATTGAGTTGATGATGAGCAATCTGAGTATGAGACTTCGAAACAAATGACT 107
DB 1252 AAAGATTTTGTGTTTATCTGGGATTTTAAACGAAAAACGAGCCAGTGAAC 1311
QY 108 CGGAGACTACCGAGATTTATTTTGGCATTGCTCCATCAGTCCATCAGTAT 167
DB 1312 TGGTAACTTAATCATATTTATTTATTTTGTGTTTACGACGACGATTAACATTAATGAT 1371
QY 168 GCGA 171
DB 1372 CCTA 1375

RESULT 9
US-09-949-016-65898/c
; Sequence 65898, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65898
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-65898

Query Match 13.2%; Score 30.8; DB 4; Length 601;
Best Local Similarity 54.6%; Pred. No. 2;
Matches 59; Conservative 1; Mismatches 48; Indels 0; Gaps 0;
QY 2 TTTTGCAGTTAGTGAATATGTTAGTGCCTCTATGATGAGGTGAGATTGAGTTA 61
DB 376 TATTTTCTTTTAAAGATATGTTACTTCTGTGTACAGCTGAAACATTTAAAAA 317
QY 62 TTGATGAGGCAATCTCTGATATGAGACTTCAGAAAAACATGACTCG 109
DB 316 AAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 269

RESULT 10
US-09-918-686-1/c
; Sequence 1, Application US/09318686
; Patent No. 6475739
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary
; APPLICANT: Prohl, Sean
; APPLICANT: Paepfer, Bryan
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; FILE REFERENCE: 240083.515
; CURRENT APPLICATION NUMBER: US/09/918,686
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 92139
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7043, 8369, 8401
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

Query Match 13.1%; Score 30.6; DB 4; Length 92139;
Best Local Similarity 68.9%; Pred. No. 23;
Matches 42; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 114 GCTACCGAGATTTATTTATTTGATGCTCTCCATCAGTCTACCATCAGTATGCGAGA 173
DB 71386 GCTTGACATGATTCCTTGTCTGGAATTCCTCCATGAGGATCCCATTCCTGCTGAGA 71327
QY 174 T 174
DB 71326 T 71326

RESULT 11
US-09-949-016-16923
; Sequence 16923, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16923
; LENGTH: 390416
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16923

Query Match 13.1%; Score 30.6; DB 4; Length 390416;
Best Local Similarity 51.1%; Pred. No. 45;
Matches 72; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 13 AGTAGAATATGTTAGTGGCTCCCTATGATGAGTGAAGATTTGAGTTATGATGAGGC 72
DB 98049 AGTAGAGCTCTGAGGAGCTGAACCACTCCAGAGAAATCATCTCTTGAAGAGAGTG 98108
QY 73 AATCTGAGTATGAGACTTCAGAAAAACATGACTCGGAGAGCTACCGAGATTATTTTA 132
DB 98109 AGTGTGTAATTTAATCATCAGCAAGAACCTGTACTGAGAGCGAGAGAGCTCG 98168
QY 133 TTGGCATTCCTCCATCAGT 153
DB 98169 TTCCAAATTAATCTCCCTCAGT 98189

RESULT 12
US-09-949-016-168377
; Sequence 168377, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14

;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 168377
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-168377

Query Match 13.0%; Score 30.2; DB 4; Length 601;
Best Local Similarity 60.2%; Pred. No. 3.2;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 122 AGATTATTTTATTTGGCATGCTCCATCAGTCTACCCATCGATGCGAGATGATAGA 181
DB 211 AGACAAATATAAAGCTGATGACTCAAAAATTTACTAGATAGATACCGTATGCTTAC 270

QY 182 TCATATTCATGATGATCCATCTTC 204
DB 271 CCTATGCTTTATTTAATCTTC 293

RESULT 13

US-09-949-016-12108/c
; Sequence 12108, Application US/09949016
; Patent No. 6812339

;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 12108
;; LENGTH: 14449
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-12108

Query Match 13.0%; Score 30.2; DB 4; Length 14449;
Best Local Similarity 60.2%; Pred. No. 14;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 105 ACTCGGAGACTACCGACAGATTTATTTGGCATGCTCCATCAGTCTACCCATCAG 164
DB 5301 ACAAGTCACTATTGGTGGATTCCTTTAGCATTCCTCCATCAATGGTCAATAG 5242

QY 165 TATGCGAGATGATAGATATAT 187
DB 5241 GATGCTCAAGATTAAGCACTAT 5219

RESULT 14

US-09-949-016-16483/c
; Sequence 16483, Application US/09949016
; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 16483
;; LENGTH: 29628
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-16483

Query Match 13.0%; Score 30.2; DB 4; Length 29628;
Best Local Similarity 60.2%; Pred. No. 19;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 122 AGATTATTTTATTTGGCATGCTCCATCAGTCTACCCATCAGATGATGCGAGATGATAGA 181
DB 3410 AGACAAATATAAAGCTGATGACTCAAAAATTTACTAGATAGATACCGTATGCTTAC 3351

QY 182 TCATATTCATGATGATCCATCTTC 204
DB 3350 CCTATGCTTTATTTAATCTTC 3328

RESULT 15

US-09-949-016-14856/c
; Sequence 14856, Application US/09949016
; Patent No. 6812339

;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 14856
;; LENGTH: 63385
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(63385)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14856

Query Match 12.9%; Score 30; DB 4; Length 63385;
Best Local Similarity 53.4%; Pred. No. 31;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 36 ATGATAGGATGGAAGATTTGATTTGATGAGGCAATCTGTGATGAGACTTCAG 95
DB 18045 ATGGAGGGATGCACTTTTAGAGGGGTGGGGAGCGCTTCACTAGAGAGGGCATTTG 17986

QY 96 AAACATGACTCGGGAAGCTACCGACATTTATTTATTTGGCATGCTCCATCAGT 153
DB 17985 CACAAAGACCGGAGGAGGCAAAATTTAAACGAAAGTTGCATGCTGTAGCAGT 17928

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Thu May 5 18:28:54 2005

us-09-300-482-1.rn1

Page 6

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OM nucleic - nucleic search, using sw model

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5591.830 Million cell updates/sec

Title: US-09-300-482-27

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/pdata/1/ina/6A.COMB.seq:
3: /cgn2_6/pdata/1/ina/6B.COMB.seq:
4: /cgn2_6/pdata/1/ina/6B.COMB.seq:
5: /cgn2_6/pdata/1/ina/PCTUS.COMB.seq:
6: /cgn2_6/pdata/1/ina/Backfile1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58.6	25.6	253	US-09-313-294A-6236	Sequence 6236, Ap
2	57.6	25.2	277	US-09-313-294A-4756	Sequence 4756, Ap
3	43.8	19.1	294	US-09-313-294A-5508	Sequence 5508, Ap
4	32.4	14.1	128516	US-09-949-016-13501	Sequence 13501, A
5	32.4	14.1	133157	US-09-949-016-12541	Sequence 12541, A
6	32	14.0	385	US-09-513-999C-23635	Sequence 23635, A
7	31.8	13.9	601	US-09-949-016-79076	Sequence 79076, A
8	31.8	13.9	163181	US-09-949-016-13730	Sequence 13730, A
9	31.8	13.9	211049	US-09-949-016-15770	Sequence 15770, A
10	31.8	13.9	784019	US-09-949-016-14033	Sequence 14033, A
11	31.8	13.9	828152	US-09-949-016-12777	Sequence 12777, A
12	31.6	13.8	7151	US-09-839-477-7	Sequence 7, Appl
13	31.2	13.6	2523	US-09-614-221A-346	Sequence 346, App
14	31.2	13.6	225127	US-09-949-016-16480	Sequence 16480, A
15	31.2	13.6	1830121	US-09-557-884-1	Sequence 1, Appl
16	31.2	13.6	1830121	US-09-643-990A-1	Sequence 1, Appl
17	31	13.5	601	US-09-949-016-195151	Sequence 195151, A
18	31	13.5	57331	US-09-949-016-17277	Sequence 17277, A
19	30.8	13.4	152583	US-09-949-016-12086	Sequence 12086, A
20	30.8	13.4	152583	US-09-949-016-17390	Sequence 17390, A
21	30.8	13.4	152583	US-09-949-016-17391	Sequence 17391, A
22	30.8	13.4	1230025	US-09-198-452A-1	Sequence 1, Appl
23	30.8	13.4	1230230	US-09-438-185A-1	Sequence 1, Appl
24	30.6	13.4	2454	US-09-248-796A-6173	Sequence 6173, Ap
25	30.6	13.4	640681	US-09-790-988-1	Sequence 1, Appl
26	30.4	13.3	1026	US-09-149-624-1	Sequence 1, Appl
27	30.4	13.3	15249	US-08-956-171B-102	Sequence 102, App

c	28	30.4	13.3	15249	4	US-08-781-986A-102	Sequence 102, App
c	29	30	13.1	286	4	US-09-313-294A-6591	Sequence 6591, Ap
c	30	30	13.1	400	3	US-09-222-938A-3	Sequence 3, Appl
c	31	29.6	12.9	996	4	US-09-328-352-3814	Sequence 3814, Ap
c	32	29.6	12.9	1152	3	US-09-134-001C-592	Sequence 592, App
c	33	29.6	12.9	1435	5	PCT-US95-05922A-1	Sequence 1, Appl
c	34	29.6	12.9	1601	4	US-09-023-655-497	Sequence 497, App
c	35	29.6	12.9	2580	2	US-08-511-485-7	Sequence 7, Appl
c	36	29.6	12.9	2580	4	US-09-201-936-7	Sequence 7, Appl
c	37	29.6	12.9	2580	4	US-09-011-356-7	Sequence 7, Appl
c	38	29.6	12.9	2580	4	US-09-672-717-222	Sequence 222, App
c	39	29.6	12.9	2580	4	US-09-201-932-7	Sequence 7, Appl
c	40	29.6	12.9	2589	3	US-08-569-749-1	Sequence 1, Appl
c	41	29.6	12.9	2589	4	US-09-689-356-1	Sequence 1, Appl
c	42	29.6	12.9	2589	5	PCT-US96-12860-1	Sequence 1, Appl
c	43	29.6	12.9	3516	4	US-09-710-279-3533	Sequence 3533, Ap
c	44	29.6	12.9	3532	2	US-09-205-204-1	Sequence 1, Appl
c	45	29.6	12.9	3732	3	US-09-212-971-7	Sequence 7, Appl

ALIGNMENTS

```

RESULT 1
US-09-313-294A-6236
Sequence 6236, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalqudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 6236
LENGTH: 253
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700351460H1
US-09-313-294A-6236

Query Match      25.6%; Score 58.6; DB 4; Length 253;
Best Local Similarity 66.4%; Pred. No. 2.4e-10;
Matches: 99; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY      65 ACAAGATAGGCTTGTGATGCTGTATATGGCAAAATCTGGCACTCAATATTGCT 124
DB      82 ACAAGATCGGCTTGTGCTTGGCTTGGCAATGGGCAAGAACTTGCCTCAACTTGA 141

QY      125 TGAAGAGGCTTCCCAATTCGGTTAACAAGCAACCATTTCCAGGTTATGGGCCATA 184
DB      142 GAGAAAGGG-TTCCCCATCTGTGTACACAGCAACCTTCCAGGTGAGACAGCGT 200

QY      185 AGACGAGCAACCAAGGAAAGCACTTC 213
DB      201 GAGCGCTGCCAAGGCAAGAAAGCACTTC 229

RESULT 2
US-09-313-294A-4756
Sequence 4756, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalqudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US

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/ CURRENT APPLICATION NUMBER: US/09/313,294A
 / CURRENT FILING DATE: 1999-05-14
 / NUMBER OF SEQ ID NOS: 7600
 / SOFTWARE: PERL Program
 / SEQ ID NO 4756
 / LENGTH: 277
 / TYPE: DNA
 / ORGANISM: Zea mays
 / FEATURE:
 / NAME/KEY: misc feature
 / OTHER INFORMATION: Incyte ID No. 6476212 700348987H1
 / LOCATION: 2, 72, 88
 / OTHER INFORMATION: a, t, c, g, or other
 / US-09-313-294A-4756

Query Match 25.2%; Score 57.6; DB 4; Length 277;
 Best Local Similarity 65.8%; Pred. No. 5.5e-10;
 Matches 98; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

QY 65 ACAAGATAGGCTTGTGATGCTGTTAATGGCAAAATCTGCACATCATTTGCT 124
 DB 82 ACAAGATCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 141
 QY 125 TGAAGAGGCTTCCCAATTCGTTAAACAAGCAATTCCTCAAGTTATGGCCAT 184
 DB 142 GAGAAAGG-TCCTCCATCTCTGTGTACAACAGAACCTCCAGGTGACGACCGT 200
 QY 185 AGACGAGCAACCAAGGAGAAACCTTC 213
 DB 201 GACGCTGCCAAGGACAGAAACCTTC 229

RESULT 3
 / US-09-313-294A-5508
 / Sequence 5508, Application US/09313294A
 / Patent No. 6476212
 / GENERAL INFORMATION:
 / APPLICANT: Lalagudi, Raghunath V.
 / APPLICANT: Ito, Laura Y.
 / TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 / FILE REFERENCE: PL-0017 US
 / CURRENT APPLICATION NUMBER: US/09/313,294A
 / CURRENT FILING DATE: 1999-05-14
 / NUMBER OF SEQ ID NOS: 7600
 / SOFTWARE: PERL Program
 / SEQ ID NO 5508
 / LENGTH: 294
 / TYPE: DNA
 / ORGANISM: Zea mays
 / FEATURE:
 / NAME/KEY: misc feature
 / OTHER INFORMATION: Incyte ID No. 6476212 700350270H1
 / NAME/KEY: unsure
 / LOCATION: 51
 / OTHER INFORMATION: a, t, c, g, or other
 / US-09-313-294A-5508

Query Match 19.1%; Score 43.8; DB 4; Length 294;
 Best Local Similarity 60.4%; Pred. No. 3.4e-05;
 Matches 90; Conservative 0; Mismatches 57; Indels 2; Gaps 1;

QY 75 GCCTTGCTGATTTGCTGTTATGGGCAAAATCTGCACATCATTTGCTGTTAAAGG 134
 DB 145 GCCTGCGCGGCTGCGGTATGAGACAACTTGCCTCAACATGCGGAGAAAGGT 204
 QY 135 TTCCCAATTCGGTTAAACAAGCAATTCCTCAAGTTATGGGCGCATTAAGCAAGA 194
 DB 205 TCCTCATCTGGTTAAACAAGCA--CAACTCAAGGTGTATGAGACGTCGACGCGTCC 262
 QY 195 AACGAGAGAAACCTTCATTTATGGG 223

DB 263 AAGTCGAGAGAACTCCCATGTTTGG 291

RESULT 4
 / US-09-949-016-13501
 / Sequence 13501, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 / FILE REFERENCE: CL001307
 / CURRENT APPLICATION NUMBER: US/09/949,016
 / CURRENT FILING DATE: 2000-04-14
 / PRIOR APPLICATION NUMBER: 60/241,755
 / PRIOR FILING DATE: 2000-10-20
 / PRIOR APPLICATION NUMBER: 60/237,768
 / PRIOR FILING DATE: 2000-10-03
 / PRIOR APPLICATION NUMBER: 60/231,498
 / PRIOR FILING DATE: 2000-09-08
 / NUMBER OF SEQ ID NOS: 207012
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 13501
 / LENGTH: 128516
 / TYPE: DNA
 / ORGANISM: Human
 / US-09-949-016-13501

Query Match 14.1%; Score 32.4; DB 4; Length 128516;
 Best Local Similarity 48.9%; Pred. No. 6.4;
 Matches 87; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 26 CTTCAATTCAGAGATTAATTATGCGCTCAACCCACACAGAAATAGCCCTTGCTGCA 85
 DB 16045 CTTGATACCTGACCAAGTATGAGAAATGATCCGCCCTCATGTGCTGTTAA 16104
 QY 86 TTGCTGTATATGGGCAAAATCTGGCACTCAATATGCTTTGAAAGGCTTCCCAATTC 145
 DB 16105 GTGAGAGGAATGCAAAATATGTCCTGCTATTTAAGTGAAGGACTTGCACAGGTC 16164
 QY 146 GGTAAACAGGAACCAATTCCTCAAGTTATGCGCCATTAAGAGCAACCAAGCA 203
 DB 16165 ATGCACAAAGTGGCAATGTAATTTTAAACTGACGAGATTTGAAACATGTGTA 16222

RESULT 5
 / US-09-949-016-12541
 / Sequence 12541, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 / FILE REFERENCE: CL001307
 / CURRENT APPLICATION NUMBER: US/09/949,016
 / CURRENT FILING DATE: 2000-04-14
 / PRIOR APPLICATION NUMBER: 60/241,755
 / PRIOR FILING DATE: 2000-10-20
 / PRIOR APPLICATION NUMBER: 60/237,768
 / PRIOR FILING DATE: 2000-10-03
 / PRIOR APPLICATION NUMBER: 60/231,498
 / PRIOR FILING DATE: 2000-09-08
 / NUMBER OF SEQ ID NOS: 207012
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 12541
 / LENGTH: 133157
 / TYPE: DNA
 / ORGANISM: Human
 / US-09-949-016-12541

Query Match 14.1%; Score 32.4; DB 4; Length 133157;
 Best Local Similarity 48.9%; Pred. No. 6.5;
 Matches 87; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 26 CTTCAATTTCAGGAGTTAATATGCGCTCAACCCACAGAAATAGCCTTGCTGA 85
 DB 16031 CTTGATACCTGACCAAGGATGAGAAATGGATCCGACCTGCTGCTTTAA 16090
 QY 86 TTGGCTGTTAATGGGCAAAATCTGGCACTCATATTTGTTGAAAAGGGCTCCCAATCC 145
 DB 16091 GTGGAAGGAAATGTGCAATTTATGTCCTGCTATTCTTAAGTGAAGAGACTTGCCCAAGTTC 16150
 QY 146 GGTTAACAACGAGAACCATTTCCAGGTTAATTTGGCCATTAAGAAGAACCAACAGGAA 203
 DB 16151 ATGCAACAAGTTGGCAATGTAATTTTAAACTGAGACAGATGTTGAAAACATGCTA 16208

RESULT 6
 US-09-513-999C-23635
 ; Sequence 23635, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duclet, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6783961
 ; FILE REFERENCE: 59, US2, REG
 ; CURRENT APPLICATION NUMBER: US/09/513, 999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 23635
 ; LENGTH: 385

; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 13
 ; OTHER INFORMATION: w=a or t
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 98
 ; OTHER INFORMATION: n=a, g, c or t
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 99
 ; OTHER INFORMATION: h=a or c or t
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 151
 ; OTHER INFORMATION: m=a or c
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 152
 ; OTHER INFORMATION: m=a or c
 ; US-09-513-999C-23635

Query Match 14.0%; Score 32; DB 4; Length 385;
 Best Local Similarity 51.4%; Pred. No. 0.48;
 Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 9 ATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAAATATGCGCTCAACCCACAA 68
 DB 242 ATTTGTTTATTTGCTTGGGAGAGGATTTTAAATATTTTGGCTTAATCAA 301
 QY 69 GAATAGGCTTCTGATGCTGTTAATGGGCAAAATCTGGCACTCATATTTGCTGA 128
 DB 302 GAAGTCCCTCTGAGATGTTAATTTTAAATGTCAAAATGATGAACGATATATCTTGA 361
 QY 129 AAGGCTTCCCAATTCGGTTAAC 152
 DB 362 AGTGAATTCGAATATGCTTAAC 385

RESULT 7
 US-09-949-016-79076/c
 ; Sequence 79076, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 79076
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-79076

Query Match 13.9%; Score 31.8; DB 4; Length 601;
 Best Local Similarity 64.0%; Pred. No. 0.71;
 Matches 48; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2 AGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAAATATGCGCTCAACCC 61
 DB 528 AAAGCAATTTTCTGATTTGCTTCAATTTGAGATTAATATGCTGAGCTCAATAT 469
 QY 62 ACAACAGATATAGC 76
 DB 468 ACACTGAATATAGC 454

RESULT 8
 US-09-949-016-13730
 ; Sequence 13730, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13730
 ; LENGTH: 163181
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(163181)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-949-016-13730

Query Match 13.9%; Score 31.8; DB 4; Length 163181;
 Best Local Similarity 53.7%; Pred. No. 12;
 Matches 66; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
 QY 103 AATCTGCACTCATATTTGTTGAAGGCTTCCCAATTCGGTTAACAAGGAGACA 162

Db 140224 AAATTGAGGTGATCATGTAATGAAAGCTTGCATTTATGAGGCAACACACAGG 140283
QY 163 TTTCAGAGTTATTTGGGCCATTAAGACGAAGCAACAGAGAAAGAACTTCAATTTATGG 222
Db 140284 CTGAAACAGATTTTACAGACAGATACAGGACACAGAGAAAGAACTTCAATTTATGG 140343
QY 223 GGA 225
Db 140344 AGA 140346

RESULT 9
US-09-949-016-15770/C
; Sequence 15770, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 15770
; LENGTH: 211049
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15770

Query Match
Best Local Similarity 13.9%; Score 31.8; DB 4; Length 211049;
Matches 81; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 2 AGACCTTATTTTCTGTCATTTGCTTCAATTTTCAGAGATTAATTAATGCGCTCAACC 61
Db 22914 AAATGTTGATTAATAGAGCGTTTGTACAAATTTGAGAAATGAGGACCTGCTTAGTGC 22855
QY 62 ACAACAGAAATGAGCGCTTCTGATTTGCTGTAATGAGCAAAATCTGCACTCAATAT 121
Db 22854 AAAATGTTGATTTTACACTAGATTTGCTTATATTTGGTAAATAATTTCTGCAGTATA 22795
QY 122 GCTTGAAGAGGCTTCCCAATTCGGTTTACACGAAACCAATT 164
Db 22794 ATTTCAAATGATTTACACTTATATGAGTAAACCAATTACCACT 22752

RESULT 10
US-09-949-016-14033/C
; Sequence 14033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 14033
; LENGTH: 784019
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(784019)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14033

Query Match
Best Local Similarity 13.9%; Score 31.8; DB 4; Length 784019;
Matches 48; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2 AGACCTTATTTTCTGTCATTTGCTTCAATTTTCAGAGATTAATTAATGCGCTCAACC 61
Db 474638 AAAGCAGATTTTCTTGAATTTGCTTCAATTTGGAATTAATGTTGGGCTCAATAT 474579
QY 62 ACAACAGAAATGAGC 76
Db 474578 ACACTGAATATGAC 474564

RESULT 11
US-09-949-016-12777/C
; Sequence 12777, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12777
; LENGTH: 828152
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(828152)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12777

Query Match
Best Local Similarity 13.9%; Score 31.8; DB 4; Length 828152;
Matches 48; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2 AGACCTTATTTTCTGTCATTTGCTTCAATTTTCAGAGATTAATTAATGCGCTCAACC 61
Db 470771 AAAGCAGATTTTCTTGAATTTGCTTCAATTTGGAATTAATGTTGGGCTCAATAT 470712
QY 62 ACAACAGAAATGAGC 76
Db 470711 ACACTGAATATGAC 470697

RESULT 12
US-09-839-477-7
; Sequence 7, Application US/09839477
; Patent No. 6723895
; GENERAL INFORMATION:
; APPLICANT: Shortosh, Basil S.
; APPLICANT: DeBonte, Lorin R.
; TITLE OF INVENTION: PLANTS CONTAINING A CYTOSOLIC ACETYL

FILE OF INVENTION: COA-CARBOXYLASE
FILE REFERENCE: 07148-094001
CURRENT APPLICATION NUMBER: US/09/839,477
CURRENT FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: US 60/198,794
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 7
LENGTH: 7151
TYPE: DNA
ORGANISM: Medicago sativa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(6771)
US-09-839-477-7

Query Match 13.8%; Score 31.6; DB 4; Length 7151;
Best Local Similarity 54.2%; Pred. No. 2.9;
Matches 64; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 54 CTCACCCCAACAAGATAGGCTTGCTGATGGCTGTTATGGCAAAATCTGGCAC 113
DB 5807 CTGATTCGCGACCAAGCGCCCAAGCATATTGATTTCAAGAGAAGACTCCAC 5866

QY 114 TCAATATTCCTGAAAAGGCTTCCCAATTCGGTTAACACGGAACCATTTCCAAAG 171
DB 5867 TTTTCATTATCCCAACTGAGAGGCTTTCAGGTGACGAAGGACCTTTTGAAGG 5924

RESULT 13
US-09-614-221A-346
Sequence 346, Application US/09614221A
Patent No. 6723837
GENERAL INFORMATION:
APPLICANT: Karunananda, Balasubramanian
APPLICANT: Yu, Jaehyun
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
FILE REFERENCE: 16516.075
CURRENT APPLICATION NUMBER: US/09/614,221A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/142,981
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 626
SEQ ID NO 346
LENGTH: 2523
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-346

Query Match 13.6%; Score 31.2; DB 4; Length 2523;
Best Local Similarity 55.6%; Pred. No. 2.3; 48; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 69 GATAGGCTTCTGATGGCTGTTAATGGCAAAATCTGGCACTCAATATTGCTTGAA 128
DB 2305 GGATGGGACTTCTGATTTAAATAGTACGCGAAAGTACCTATATTACCAATTTTG 2364

QY 129 AAGGCTTCCCAATTCGGTTAACACGGAACCATTTCCAAAGTTT 176
DB 2365 AAGGCTACCAATTCATGAAAACAAAGTAAAGATCAACAAGTTT 2412

RESULT 14
US-09-949-016-16480
Sequence 16480, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16480
LENGTH: 225127
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(225127)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16480

Query Match 13.6%; Score 31.2; DB 4; Length 225127;
Best Local Similarity 54.3%; Pred. No. 22;
Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 93 TTAATGGCAAAATCTGGCACTCATATTGCTTGAAAAGGCTTCCCAATTCGGTTAAC 152
DB 16067 TTTAAAAGCACAGAGTGGCAAGCTGATATAAAAGCAAGACCAACCAATTGCTGTTC 16126

QY 153 AAGGACCATTTCCAAAGTTTATGGGCGCATTAAGACGAAGCAACAGAGAGAA 208
DB 16127 ATGAGACCAATTTCAATGATATGTTATGTTACCCACAGCGCAAGTAAAGATGAGAG 16182

RESULT 15
US-09-557-884-1/C
Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs

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;
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
;      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

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Query Match      13.6%; Score 31.2; DB 4; Length 1830121;
Best Local Similarity 53.2%; Pred. No. 60;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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QY      31 AATTTCAGGAGATTATTTATGCGCTCAACCCACACAGAGATAGGCGCTTGCTGGATTGGC 90
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Db      324697 ACTTTTATATAAAAAATTTAACTTGATCACAATTTAGAAATTTGCTCTTGAGATTCTC 324638
          |||
QY      91 TGTTAATGGGCAAAATCTGCGACTCAATATTTGCTTGAAAAGGCGCTTCCCAATTCCGGTTA 150
          |||
Db      324637 TATTATTTGGCATACATTAATCTCAAAATTTAGTTGAGCGGATTTTGTCTCTACAATTTG 324578
          |||
QY      151 ACAA 154
          |||
Db      324577 ACAA 324574

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Search completed: May 4, 2005, 12:28:02
 Job time : 75.0098 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 259.813 Seconds
(without alignments)
5365.716 Million cell updates/sec

Title: US-09-300-482-27

Perfect score: 229

Sequence: 1 cagaccctattctctctc.....ctcattatcgagggaacaa 229

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	137.8	60.2	4825	US-10-424-599-59918	Sequence 59918, A
2	136.2	59.5	2691	US-10-424-599-59924	Sequence 59924, A
3	126.6	55.3	578	US-10-424-599-59920	Sequence 59920, A
4	117	51.1	1737	US-10-425-114-12849	Sequence 12849, A
5	81	35.4	1627	US-10-425-114-10641	Sequence 10641, A
6	81	35.4	1838	US-10-424-599-76904	Sequence 76904, A
7	74.2	32.4	1735	US-10-739-930-1129	Sequence 1129, Ap
8	73.8	32.2	375	US-10-424-599-98726	Sequence 98726, A
9	63.4	27.7	1125	US-10-425-115-44920	Sequence 44920, A
10	63.4	27.7	1953	US-10-767-701-14931	Sequence 14931, A
11	62.8	27.4	234	US-09-732-627A-2087	Sequence 2087, Ap

12	62	27.1	367	17	US-10-424-599-60294	Sequence 60294, A
13	60.2	26.3	1831	18	US-10-437-963-98959	Sequence 98959, A
14	58.6	25.6	637	17	US-10-425-114-12436	Sequence 12436, A
15	58.6	25.6	637	18	US-10-425-115-91011	Sequence 91011, A
16	58.6	25.6	748	18	US-10-425-115-91003	Sequence 91003, A
17	58.6	25.6	1587	17	US-10-425-114-6537	Sequence 6537, Ap
18	58.6	25.6	1624	17	US-10-425-114-30841	Sequence 30841, A
19	58.6	25.6	1650	17	US-10-425-114-3149	Sequence 3149, Ap
20	58.6	25.6	1661	17	US-10-425-114-24375	Sequence 24375, A
21	58.6	25.6	1669	17	US-10-425-114-15154	Sequence 31534, A
22	58.6	25.6	1671	17	US-10-425-114-1523	Sequence 1523, Ap
23	58.6	25.6	1672	17	US-10-425-114-24039	Sequence 24039, Ap
24	58.6	25.6	1672	17	US-10-425-114-32227	Sequence 32227, A
25	58.6	25.6	1674	17	US-10-425-114-13683	Sequence 13683, A
26	58.6	25.6	1675	17	US-10-425-114-446	Sequence 446, App
27	58.6	25.6	1678	17	US-10-425-114-4238	Sequence 4238, Ap
28	58.6	25.6	1678	17	US-10-425-114-13558	Sequence 13538, A
29	58.6	25.6	1678	17	US-10-425-114-24256	Sequence 24256, A
30	58.6	25.6	1678	17	US-10-425-114-25038	Sequence 25038, A
31	58.6	25.6	1681	17	US-10-425-114-4096	Sequence 4096, Ap
32	58.6	25.6	1684	17	US-10-425-114-5153	Sequence 25153, A
33	58.6	25.6	1684	17	US-10-425-114-3615	Sequence 3615, Ap
34	58.6	25.6	1691	17	US-10-425-114-28011	Sequence 28011, A
35	58.6	25.6	1728	17	US-10-425-114-4434	Sequence 4434, Ap
36	58.6	25.6	1740	17	US-10-425-114-24479	Sequence 24479, A
37	58.6	25.6	1781	17	US-10-425-114-3294	Sequence 3294, Ap
38	58.6	25.6	1798	17	US-10-425-114-508	Sequence 508, App
39	58.6	25.6	1798	17	US-10-425-114-1418	Sequence 1418, Ap
40	58.6	25.6	1872	17	US-10-425-114-26662	Sequence 26662, A
41	58.6	25.6	2171	17	US-10-425-114-2633	Sequence 2633, Ap
42	58.6	25.6	2469	18	US-10-425-115-91000	Sequence 91002, A
43	58.6	25.6	3520	18	US-10-425-115-91000	Sequence 91000, A
44	57.4	25.1	1755	17	US-10-425-114-12333	Sequence 32383, A
45	57.4	25.1	1776	17	US-10-425-114-3640	Sequence 3640, Ap

ALIGNMENTS

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RESULT 1
US-10-424-599-59918
; Sequence 59918, Application US/10424599
; Publication NO. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement
; FILE REFERENCE: 38-21153223/B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 59918
; LENGTH: 4825
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25117C.1
US-10-424-599-59918
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Query Match 60.2%; Score 137.8; DB 17; Length 4825;
Best Local Similarity 80.8%; Pred. No. 9.9e-34;
Matches 185; Conservative 0; Mismatches 42; Indels 2; Gaps 2;

QY	1	CAGACCTATTCTTCTGCAATTCCTCAATTCAGAGATTATATGCGCTCAACC	60
DB	2331	CAGACCTATTCTTCTGCAATTCCTCAATTCAGAGATTATATG-GCTCAACC	2389
QY	61	CACACAGAAATAGGCTTGCTGATGCTGTATATGGGCAAAATCGGCACTCAATAT	120
DB	2390	CTCAACAGAAATAGGCTTGCTGATGCTGTATATGGGCAAAATCTAGCACTCAATAT	2449

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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(578)
; OTHER_INFORMATION: unsure at all n locations
; FEATURE:
; OTHER_INFORMATION: CLONE ID: PAT_MRI3847_25119C.1
US-10-424-599-59920

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Best Local Similarity	77.7%	Pred. No. 1.6e-30;	Length 5/8;
Matches 178; Conservative	0;	Mismatches 49;	Indels 2; Gaps 2;

QY	1	CAGACCTTATTTTCTGTCATTTGCTCAAAATTCAGAGATTTAATTATGGCTCAACC	60
Db	216	CACACCTTATTTTCTCTCATTCATTCGTTCAAAATTCAGAAATTCATTTATG-GCTCAACC	274
QY	61	CACAAACAATAATAGGCTGTGCGATTTGGCTGTTAATGGCCAAATTCGGCACTCAATAT	120
Db	275	CTCAACAATAATAGGCTGTGCTGTGACATGGCCCTTAATGGCCAAAATTCAGCACTCAATAT	334
QY	121	TGCTGAAAAAGGCTTCCCAATTCGCGTTAACAGACGAACCATTTCCAGATTTATGGGC	180
Db	335	TGCG-TGAGGCAAGCTTTCCTCATTTCTGTGTATTAACGAACCACTTCCAGATGTATGAGA	393
QY	181	CATTAAGACGAACCAACAACGAGAGAGAAATCTTCATTTATGGGGAACA	229
Db	394	CTGTGAAACGACGAACAACAAGAGAAATCTTCCAGTTATGGCTACCA	442

RESULT 4
RS-S-10-425-114-12849

Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tadaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 12849
LENGTH: 1737
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701214664.1

Query Match	51.1%;	Score 117;	DB 17;	Length 1737;
Best Local Similarity	81.2%;	Pred. No. 3.5e-27;		
Matches 160;	Conservative 0;	Mismatches 35;	Indels 2;	Gaps 2;
33	TTTCAGAGATTAA	TTATGCGCTCAACCCACAACAAGATTAGCGCTTGCTGATTTGGCTG	92	
43	TATCTGAGTTAT	TATATG-GCTCAACCCACAACAAGATTAGCGCTTGCTGATTTGGCTG	101	
93	TTATATGGGCAAAATCTGGCACTCAATATTTGCTTGA	AAAGGCTTCCCAATTCGCGTTAC	152	
102	TTATATGGGCCAAATCTGGCACTCAATATTTG-C-TGA	AAAGGCTTTCCTTCCATTTCTGTTTAC	160	
153	AACGGAACCATTTCCAAAGGTTATTTGGCCATAAGACGAAGCAAAACGAGAGAAACCTT	212		
161	AACGGAACCATTTCCAAAGGTTGATGACAGTAGAAGCAAGCAAAACAAGAAAGAAATCTT	220		
213	CAATTTATGGGGACAA	229		

RESULT 5
US-10-425-114-10641
; Sequence 10641, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10641
; LENGTH: 1627
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700954712_FLI
US-10-425-114-10641

Query Match 35.4%; Score 81; DB 17; Length 1627;
Best Local Similarity 72.1%; Pred. No. 1.7e-15;
Matches 119; Conservative 0; Mismatches 45; Indels 1; Gaps 1;

QY 65 ACAAGATGGCTTCTGATGCTGTTAATGGCAAAATCTGGCACTCAATATGCT 124
DB 71 ACAAGATGGCTTCTGCTGCTGCTGATGGGCAAACTTCTCAACATTCG- 129

QY 125 TCAAAAGGCTTCCCAATTCGGTTAACAAGGAACCATTTTCAAGTTATGGCCATA 184
DB 130 TGAGAAAGGCTTCCCATTTCTGTCTACACCGGACCGGCTCCAGGTTGATGACAGT 189

QY 185 AGACGAGCAACCAAGAGAAACCTTCATTTATGGGAAACA 229
DB 190 TGAAGAGCAAAACAAGAGAAACCTTCTGTGTATGCTACCA 234

RESULT 6
US-10-424-599-76904
; Sequence 76904, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 76904
; LENGTH: 1838
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40459C.1
US-10-424-599-76904

Query Match 35.4%; Score 81; DB 17; Length 1838;
Best Local Similarity 72.1%; Pred. No. 1.8e-15;
Matches 119; Conservative 0; Mismatches 45; Indels 1; Gaps 1;

QY 65 ACAAGATGGCTTCTGATGCTGTTAATGGCAAAATCTGGCACTCAATATGCT 124
DB 71 ACAAGATGGCTTCTGCTGCTGCTGATGGGCAAACTTCTCAACATTCG- 129

DB 224 ACAAGATAGGCTTCTGCTGCTGCTGATGGGCCAAACCTTCTCTCAACATTCG- 282

QY 125 TCAAAAGGCTTCCCAATTCGGTTAACAAGGAACCATTTTCAAGTTATGGCCATA 184
DB 283 TGAGAAAGGCTTCCCATTTCTGTCTACACCGGACCGGCTCCAGGTTGATGACAGT 342

QY 185 AGACGAGCAACCAAGAGAAACCTTCATTTATGGGAAACA 229
DB 343 TGAAGAGCAAAACAAGAGAAACCTTCTGTGTATGCTACCA 387

RESULT 7
US-10-739-930-1129
; Sequence 1129, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 1129
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: ARATH-23APR03-CLUSTER6852_1
US-10-739-930-1129

Query Match 32.4%; Score 74.2; DB 18; Length 1785;
Best Local Similarity 68.4%; Pred. No. 2.9e-13;
Matches 117; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

QY 53 GCTCAACCACAAAGAATAGGCTTCTGATGGCTGTTAATGGCAAAATCTGCGA 112
DB 110 GCTGTCAACCTTACAGANTAGGCTTAGCTGACTGCTGTATGGGTGACAACTAGT 169

QY 113 CTCATATTTGCTTGAAGAGGCTTCCCAATTCGGTTAACAAGCAACCATTTCAAGT 172
DB 170 CTCACATTTGCA-GAGAAAGGCTTCCCAATTCGTTTACACAGAACTTCCAAAGT 228

QY 173 TATTGGCCATTAAGACGAGCAACCAAGAGAAACCTTCATTTATGGG 223
DB 229 TGATGAGACCGTGAAGAGCAAGCCAAAGAGGCAATCTTCTCTTACGG 279

RESULT 8
US-10-424-599-98726
; Sequence 98726, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 98726
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_60162C.1
US-10-424-599-98726

Query Match 32.2%; Score 73.8; DB 17; Length 375;
Best Local Similarity 63.2%; Pred. No. 1.9e-13;

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO: 60294
LENGTH: 367
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_25457C.1
US-10-424-599-60294

Query Match 27.1%; Score 62; DB 17; Length 367;
Best Local Similarity 66.4%; Pred. No. 1.3e-09;
Matches 89; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 65 ACAAGATAGGCGCTTGGCTGATGCTGTTAATGGGCAAAATCTGGCACTCAATATTGCT 124
DB 184 ACAAGATAGGCGCTTGGCTGATGCTGTTAATGGGCAAAATCTGGCTTAACTTGTCT 243
QY 125 TGAAGAGGCGCTTCCCAATTCGGGTTAACAACGGAACCAATTCGAGTTATTGGGCCATA 184
DB 244 GAAAGAGGCGCTTTCATTTTGTCTACACCGGACCGGCGCTCAAGGTTATGAGACAGCT 303
QY 185 AGACGACGCAACC 198
DB 304 CGATGAGCAATTC 317

RESULT 13

US-10-437-963-98959
Sequence 98959, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO: 98959
LENGTH: 1831
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_96817C.1
US-10-437-963-98959

Query Match 26.3%; Score 60.2; DB 18; Length 1831;
Best Local Similarity 64.2%; Pred. No. 1.1e-08;
Matches 106; Conservative 0; Mismatches 58; Indels 1; Gaps 1;

QY 65 ACAAGATAGGCGCTTGGCTGATGCTGTTAATGGGCAAAATCTGGCACTCAATATTGCT 124
DB 88 ACTAAGATAGGCGCTTGGCTGATGCTGTTAATGGGCAAAATCTGGCTTAACTTGTCT 147
QY 125 TGAAGAGGCGCTTCCCAATTCGGGTTAACAACGGAACCAATTCGAGTTATTGGGCCATA 184

DB 148 GAGAAAGG-TTCCCTATCTGTCTACACGACGACCTTAAAGTTGATGAGCGCT 206
QY 185 AGACGACGCAACCAGGAAGAACCTTCAATTTATGGGCAACA 229
DB 207 TCAGCGCGCAAGGTAGAGGAACCTTCCTGTGTACGGGTCCA 251

RESULT 14

US-10-425-114-12436
Sequence 12436, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO: 12436
LENGTH: 637
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 701176801_FLI
US-10-425-114-12436

Query Match 25.6%; Score 58.6; DB 17; Length 637;
Best Local Similarity 66.4%; Pred. No. 2.1e-08;
Matches 99; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY 65 ACAAGATAGGCGCTTGGCTGATGCTGTTAATGGGCAAAATCTGGCACTCAATATTGCT 124
DB 164 ACAAGATAGGCGCTTGGCTGATGCTGTTAATGGGCAAAATCTGGCTTAACTTGTCT 223
QY 125 TGAAGAGGCGCTTCCCAATTCGGGTTAACAACGGAACCAATTCGAGTTATTGGGCCATA 184
DB 224 GAGAAAGG-TTCCCTATCTGTCTACACGACGACCTTCAAGGTTATGAGACAGCT 282
QY 185 AGACGACGCAACCAGGAAGAACCTTC 213
DB 283 GCAGCGTGCAGGAGGAGGAACCTTC 311

RESULT 15

US-10-425-115-91011
Sequence 91011, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO: 91011
LENGTH: 637
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_183003C.1
US-10-425-115-91011

Query Match 25.6%; Score 58.6; DB 18; Length 637;

Best Local Similarity 66.4%; Pred. No. 2.1e-08;
 Matches 99; Conservative 0; Mismatches 49; Indels 1; Gaps 1;
 QY 65 ACAAGAAATAGGCTTGTGCTGATTTGCTGTTATGGCAAAATCTGGCACTCAATATTGCT 124
 Db 164 ACAAGAAATCGGCTTGTGCTGCTGCGCTCATGGGCGAAGAACTTGCCCTCAACATTGCA 223
 QY 125 TGAAGAAGGCTTCCCAATTCCGGTTAAACAGGAAACCAATTTCAGAGTTAATGGCCATA 184
 Db 224 GAGAAAGGG-TTCCCAATCTCTGTGTACAAACAGGAAACCTCCAGGTGAGCGAGACCGT 282
 QY 185 AGACGAAGCAAAACGAGAGGAAACCTTC 213
 Db 283 GCACCGTCCAGGCAAGGAAACCTTC 311

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:08 ; Search time 1835.74 Seconds
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Title: US-09-300-482-27

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Searched: 45554873 seqs, 2041521753 residues

Total number of hits satisfying chosen parameters: 91109746

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	229	100.0	229	20	US-09-304-517A-181981
3	229	100.0	229	20	US-09-333-535A-6002
4	229	100.0	229	21	US-09-371-146A-181981
5	229	100.0	229	26	US-09-552-086-26409
6	229	100.0	229	29	US-09-654-617-43713
7	229	100.0	229	31	US-09-684-016-43713
8	229	100.0	229	45	US-09-985-678-181981
9	161.4	70.5	829	77	US-09-089-810-829
10	153.8	67.2	261	20	US-09-300-482-27
11	153.8	67.2	261	20	US-09-304-517A-109274
12	153.8	67.2	261	21	US-09-371-146A-109274
13	153.8	67.2	261	45	US-09-985-678-109274
14	153.8	67.2	447	37	US-09-874-708A-16025
15	153.8	67.2	447	37	US-09-874-708A-16025
16	153.8	67.2	497	30	US-09-211-750-15882
17	153.8	67.2	497	90	US-09-874-708A-18187
18	152.8	66.7	262	18	US-09-211-750-18044
19	152.8	66.7	262	44	US-09-244-000A-14731
20	152.2	66.5	259	20	US-09-978-703-14731
21	152.2	66.5	259	20	US-09-300-482-27
22	152.2	66.5	259	20	US-09-304-517A-133493
23	152.2	66.5	259	21	US-09-371-146A-133493
24	152.2	66.5	259	45	US-09-985-678-133493
25	152.2	66.5	479	37	US-09-874-708A-22353
26	151.8	66.3	259	18	US-09-211-750-22158
27	151.8	66.3	259	44	US-09-244-000A-70591
28	151.4	66.1	275	18	US-09-978-703-70591
29	151.4	66.1	275	20	US-09-244-000A-21474
30	151.4	66.1	275	20	US-09-300-482-27
31	151.4	66.1	275	20	US-09-304-517A-289993
32	151.4	66.1	275	21	US-09-371-146A-288774
33	151.4	66.1	275	44	US-09-978-703-21474
34	151.4	66.1	275	45	US-09-985-678-289993
35	151.4	66.1	275	45	US-09-985-678-289993
36	151.4	66.1	275	45	US-09-985-678-289993
37	151.4	66.1	275	45	US-09-985-678-289993
38	151.4	66.1	275	45	US-09-985-678-289993
39	151.4	66.1	275	45	US-09-985-678-289993
40	151.4	66.1	275	45	US-09-985-678-289993
41	151.4	66.1	275	45	US-09-985-678-289993
42	151.4	66.1	275	45	US-09-985-678-289993
43	151.4	66.1	275	45	US-09-985-678-289993
44	151.4	66.1	275	45	US-09-985-678-289993
45	151.4	66.1	275	45	US-09-985-678-289993

ALIGNMENTS

```
RESULT 1
US-09-300-482-27
; Sequence 27, Application US/09300482
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 04993.0031.US01/38-21(15365)B
; CURRENT FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 699
; SEQ ID NO 27
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Glycine max
US-09-300-482-27
```

Query Match 100.0%; Score 229; DB 20; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTATTCGCTCAACC 60
    |||||
DB 1 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTATTCGCTCAACC 60

QY 61 CACACAGAGATAGGCTTGTGCGATTGCGTGAATGCGGAATTCGCACTCAATAT 120
    |||||
DB 61 CACACAGAGATAGGCTTGTGCGATTGCGTGAATGCGGAATTCGCACTCAATAT 120

QY 121 TGCTTGAAGAGGCTTCCCAATTCGGTTAACACGAACTTTCAGAGTTATTCGGC 180
    |||||
DB 121 TGCTTGAAGAGGCTTCCCAATTCGGTTAACACGAACTTTCAGAGTTATTCGGC 180

QY 181 CATAGAGAGAGCAACCGAGAGAACTTCAATTTATGGGACAA 229
    |||||
DB 181 CATAGAGAGAGCAACCGAGAGAACTTCAATTTATGGGACAA 229
```

```
RESULT 2
US-09-304-517A-181981
; Sequence 181981, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 181981
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-181981
```

Query Match 100.0%; Score 229; DB 20; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTATTCGCTCAACC 60
    |||||
DB 1 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTATTCGCTCAACC 60

QY 61 CACACAGAGATAGGCTTGTGCGATTGCGTGAATGCGGAATTCGCACTCAATAT 120
    |||||
DB 61 CACACAGAGATAGGCTTGTGCGATTGCGTGAATGCGGAATTCGCACTCAATAT 120

QY 121 TGCTTGAAGAGGCTTCCCAATTCGGTTAACACGAACTTTCAGAGTTATTCGGC 180
    |||||
DB 121 TGCTTGAAGAGGCTTCCCAATTCGGTTAACACGAACTTTCAGAGTTATTCGGC 180
```


Query Match	100.0%	Score 229	DB 21	length 229
Best Local Similarity	100.0%	Pred. No. 1.3e-60		
Matches 229	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	CAGACCTATTATTTCTGTCATTTGCTTCCAATTTCAGAGACTATATATATGCGCTCAACC	60	
	1	CAGACCTATTATTTCTGTCATTTGCTTCCAATTTCAGAGACTATATATATGCGCTCAACC	60	
Db				

```

RESULT 6
US-09-654-617-43713
; Sequence 43713, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 43713
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-654-617-43713

```

Query Match	100.0%;	Score 229;	DB 29;	Length 229;
-------------	---------	------------	--------	-------------

Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
| | | | |
DB 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
| | | | |
QY 61 CACAACAGAAATAGGCGCTTGGTGGATTTGGTGAATAGGCGAAATCTGGCACTCAATAT 120
| | | | |
DB 61 CACAACAGAAATAGGCGCTTGGTGGATTTGGTGAATAGGCGAAATCTGGCACTCAATAT 120
| | | | |
QY 121 TGGTTGAAAAGGCGCTTCCCAATTCGGGTTAACAACGAAACCATTTCCAGTTATTGGGC 180
| | | | |
DB 121 TGGTTGAAAAGGCGCTTCCCAATTCGGGTTAACAACGAAACCATTTCCAGTTATTGGGC 180
| | | | |
QY 181 CATAGACGAAGCAACCAAGAGAAACCTTCAATTTATGGGAAACA 229
| | | | |
DB 181 CATAGACGAAGCAACCAAGAGAAACCTTCAATTTATGGGAAACA 229
| | | | |

RESULT 7

US-09-684-016-43713
Sequence 43713, Application US/09684016

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/684,016
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/654,617
NUMBER OF SEQ ID NOS: 2000-09-05
SEQ ID NO 43713
LENGTH: 229
TYPE: DNA
ORGANISM: Glycine max
US-09-684-016-43713

Query Match 100.0%; Score 229; DB 31; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
| | | | |
DB 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
| | | | |
QY 61 CACAACAGAAATAGGCGCTTGGTGGATTTGGTGAATAGGCGAAATCTGGCACTCAATAT 120
| | | | |
DB 61 CACAACAGAAATAGGCGCTTGGTGGATTTGGTGAATAGGCGAAATCTGGCACTCAATAT 120
| | | | |
QY 121 TGGTTGAAAAGGCGCTTCCCAATTCGGGTTAACAACGAAACCATTTCCAGTTATTGGGC 180
| | | | |
DB 121 TGGTTGAAAAGGCGCTTCCCAATTCGGGTTAACAACGAAACCATTTCCAGTTATTGGGC 180
| | | | |
QY 181 CATAGACGAAGCAACCAAGAGAAACCTTCAATTTATGGGAAACA 229
| | | | |
DB 181 CATAGACGAAGCAACCAAGAGAAACCTTCAATTTATGGGAAACA 229
| | | | |

RESULT 8

US-09-985-678-181981
Sequence 181981, Application US/09985678

GENERAL INFORMATION:
APPLICANT: Cheikh, Nordin
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 16517,255/38-21(15097)F
CURRENT APPLICATION NUMBER: US/09/985,678
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 09/304,517
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 295529

SEQ ID NO 181981
LENGTH: 229
TYPE: DNA
ORGANISM: Glycine max
US-09-985-678-181981

Query Match 100.0%; Score 229; DB 45; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
| | | | |
DB 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
| | | | |
QY 61 CACAACAGAAATAGGCGCTTGGTGGATTTGGTGAATAGGCGAAATCTGGCACTCAATAT 120
| | | | |
DB 61 CACAACAGAAATAGGCGCTTGGTGGATTTGGTGAATAGGCGAAATCTGGCACTCAATAT 120
| | | | |
QY 121 TGGTTGAAAAGGCGCTTCCCAATTCGGGTTAACAACGAAACCATTTCCAGTTATTGGGC 180
| | | | |
DB 121 TGGTTGAAAAGGCGCTTCCCAATTCGGGTTAACAACGAAACCATTTCCAGTTATTGGGC 180
| | | | |
QY 181 CATAGACGAAGCAACCAAGAGAAACCTTCAATTTATGGGAAACA 229
| | | | |
DB 181 CATAGACGAAGCAACCAAGAGAAACCTTCAATTTATGGGAAACA 229
| | | | |

RESULT 9

US-60-089-810-829
Sequence 829, Application US/60089810

GENERAL INFORMATION:
APPLICANT: Joseph R. Byrum
APPLICANT: Michael D. Thompson
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules
TITLE OF INVENTION: Associated With Plants.
NUMBER OF SEQUENCES: 5409
CORRESPONDENCE ADDRESS:
ADDRESSER: Lawrence M. Lavin, Jr.

STREET: BBAF
STREET: Monsanto Company
STREET: 700 Chesterfield Parkway North
CITY: St. Louis
STATE: MO
COUNTRY: United States
ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette (3.5in, 1.44 MB)
COMPUTER: IBM PC/XT/AT, IBM PS/2 or compatibles
OPERATING SYSTEM: Windows 95/NT
SOFTWARE: Winzip 6.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/089,810

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lavin Jr., Lawrence M.

REGISTRATION NUMBER: 30,768

REFERENCE/DOCKET NUMBER: 38-21(15395)A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 737-6670

TELEFAX: (314) 737-6047

INFORMATION FOR SEQ ID NO: 829:

SEQUENCE CHARACTERISTICS:

LENGTH: 305 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Glycine max

DEVELOPMENTAL STAGE: R3+R5 drought stressed

TISSUE TYPE: root
IMMEDIATE SOURCE:
LIBRARY: SOTMON028
CLONE: 701097624H1
US-60-089-810-829

Query Match
Best Local Similarity 70.5%; Score 161.4; DB 77; Length 305;
Matches 190; Conservative 0; Mismatches 35; Indels 2; Gaps 2;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 60
DB 38 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 96
QY 61 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAATGGGCAAAATCTGGCACTCAATAT 120
DB 97 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAATGGGCAAAATCTGGCACTCAATAT 155
QY 121 TGCCTGAAAAGGCTTCCCAATTCGGTTAAACAAGCAACCAATTCAGAGTTATTTGGGC 180
DB 156 TGCCTGAAAAGGCTTCCCAATTCGGTTAAACAAGCAACCAATTCAGAGTTATTTGGGC 215
QY 181 CATAAGACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 227
DB 216 NNGAGAACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 262

RESULT 10
US-09-300-482-70
Sequence 70, Application US/09300482
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Pesche, Virginia M.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
FILE REFERENCE: 04983.0031.US01/38-21(15365)B
CURRENT APPLICATION NUMBER: US/09/300,482
CURRENT FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 699
SEQ ID NO 70
LENGTH: 261
TYPE: DNA
ORGANISM: Glycine max
US-09-300-482-70

Query Match
Best Local Similarity 67.2%; Score 153.8; DB 20; Length 261;
Matches 195; Conservative 0; Mismatches 32; Indels 2; Gaps 2;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 60
DB 7 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 65
QY 61 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAATGGGCAAAATCTGGCACTCAATAT 120
DB 66 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAATGGGCAAAATCTGGCACTCAATAT 125
QY 121 TGCCTGAAAAGGCTTCCCAATTCGGTTAAACAAGCAACCAATTCAGAGTTATTTGGGC 180
DB 126 TGCCTGAAAAGGCTTCCCAATTCGGTTAAACAAGCAACCAATTCAGAGTTATTTGGGC 184
QY 181 CATAAGACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 229
DB 185 CAGTGAACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 233

RESULT 11
US-09-304-517A-109274
Sequence 109274, Application US/09304517A
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong

TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 38-21(15097)B
CURRENT APPLICATION NUMBER: US/09/304,517A
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 295529
SEQ ID NO 109274
LENGTH: 261
TYPE: DNA
ORGANISM: Glycine max
US-09-304-517A-109274

Query Match
Best Local Similarity 67.2%; Score 153.8; DB 20; Length 261;
Matches 195; Conservative 0; Mismatches 32; Indels 2; Gaps 2;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 60
DB 7 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 65
QY 61 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAATGGGCAAAATCTGGCACTCAATAT 120
DB 66 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAATGGGCAAAATCTGGCACTCAATAT 125
QY 121 TGCCTGAAAAGGCTTCCCAATTCGGTTAAACAAGCAACCAATTCAGAGTTATTTGGGC 180
DB 126 TGCCTGAAAAGGCTTCCCAATTCGGTTAAACAAGCAACCAATTCAGAGTTATTTGGGC 184
QY 181 CATAAGACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 229
DB 185 CAGTGAACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 233

RESULT 12
US-09-371-146A-109274
Sequence 109274, Application US/09371146A
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong
TITLE OF INVENTION: ANNOTATED PLANT GENES
FILE REFERENCE: 38-21(15097)C
CURRENT APPLICATION NUMBER: US/09/371,146A
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 09/304,517
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 294310
SEQ ID NO 109274
LENGTH: 261
TYPE: DNA
ORGANISM: Glycine max
US-09-371-146A-109274

Query Match
Best Local Similarity 67.2%; Score 153.8; DB 21; Length 261;
Matches 195; Conservative 0; Mismatches 32; Indels 2; Gaps 2;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 60
DB 7 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 65
QY 61 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAATGGGCAAAATCTGGCACTCAATAT 120
DB 66 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAATGGGCAAAATCTGGCACTCAATAT 125
QY 121 TGCCTGAAAAGGCTTCCCAATTCGGTTAAACAAGCAACCAATTCAGAGTTATTTGGGC 180
DB 126 TGCCTGAAAAGGCTTCCCAATTCGGTTAAACAAGCAACCAATTCAGAGTTATTTGGGC 184
QY 181 CATAAGACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 229
DB 185 CAGTGAACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 233

RESULT 13

Qy 1 CAGACCTTATTTTTCGTGCAATTGCCTCAAATTCAGAGATTAAATTATGGCTCAACC 60
Db 23 CAGACCTTATTTTTCGTGCAATTGCCTCAAATTCAGAGATTAAATTATG-GCTCAACC 81

Search completed: May 4, 2005, 20:13:31
Job time : 1836.74 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 92.4677 Seconds
(without alignments)
5591.850 Million cell updates/sec

Title: US-09-300-482-225

Perfect score: 316
Sequence: 1 gataagcgccgacactgag.....gattgaggagacttctga 316

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/6CTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54.8	17.3	907	US-09-620-312D-617	Sequence 617, App
2	54.8	17.3	961	US-09-620-312D-618	Sequence 618, App
3	51.8	16.4	795	US-09-248-796A-3134	Sequence 3134, Ap
4	50.4	15.9	271	US-09-313-294A-3583	Sequence 3583, Ap
5	46.2	14.6	1246	US-09-691-270A-19	Sequence 19, Appl
6	38	12.0	663	US-09-107-532A-2422	Sequence 2422, Ap
7	34.4	10.9	395	US-09-404-879A-378	Sequence 378, App
8	34.4	10.9	395	US-09-667-857-378	Sequence 378, App
9	34.4	10.9	591	US-09-854-133-314	Sequence 314, App
10	34.4	10.9	601	US-09-949-016-22949	Sequence 22949, A
11	34.4	10.9	601	US-09-949-016-22950	Sequence 22950, A
12	34.4	10.9	601	US-09-949-016-122951	Sequence 122951, A
13	34.4	10.9	601	US-09-949-016-195227	Sequence 195227, A
14	34.4	10.9	601	US-09-949-016-195228	Sequence 195228, A
15	34.4	10.9	601	US-09-949-016-195229	Sequence 195229, A
16	34.4	10.9	613	US-09-328-111-389	Sequence 389, App
17	34.4	10.9	667	US-09-328-111-388	Sequence 388, App
18	34.4	10.9	810	US-09-404-879A-206	Sequence 206, App
19	34.4	10.9	810	US-09-318-933-206	Sequence 206, App
20	34.4	10.9	810	US-09-215-681-206	Sequence 206, App
21	34.4	10.9	810	US-09-216-003A-206	Sequence 206, App
22	34.4	10.9	810	US-09-667-857-206	Sequence 206, App
23	34.4	10.9	818	US-09-949-016-5538	Sequence 5538, Ap
24	34.4	10.9	826	US-09-949-016-239	Sequence 239, App
25	34.4	10.9	1482	US-09-566-921-93	Sequence 93, Appl
26	34.4	10.9	7495	US-09-949-016-11981	Sequence 11981, A
27	34.4	10.9	7496	US-09-949-016-11280	Sequence 11280, A

C	28	34	10.8	3693	3	US-09-056-226-1	Sequence 1, Appl
	29	33.8	10.7	3639	2	US-08-737-524B-26	Sequence 26, Appl
	30	33.8	10.7	4315	4	US-09-444-905-1	Sequence 1, Appl
	31	33.4	10.6	702	4	US-09-328-352-1855	Sequence 1855, Ap
	32	33.4	10.6	263693	4	US-09-949-016-12386	Sequence 12386, A
	33	33.4	10.6	263694	4	US-09-949-016-12386	Sequence 16915, A
	34	33.2	10.5	4315	4	US-09-444-905-1	Sequence 1, Appl
	35	33	10.4	42574	4	US-09-949-016-17525	Sequence 17525, A
	36	32.8	10.4	1149	3	US-09-257-583-4	Sequence 4, Appl
	37	32.2	10.2	163022	4	US-09-949-016-16515	Sequence 16515, A
	38	32	10.1	500	4	US-09-050-739-67	Sequence 67, Appl
	39	32	10.1	1998	4	US-09-894-844-6	Sequence 69, Appl
	40	32	10.1	2050	4	US-09-050-739-69	Sequence 69, Appl
	41	32	10.1	2999	4	US-09-710-279-3482	Sequence 3482, Ap
	42	32	10.1	16885	1	US-08-390-878-16	Sequence 16, Appl
	43	32	10.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl
	44	32	10.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl
	45	31.8	10.1	601	4	US-09-949-001-760	Sequence 760, App

ALIGNMENTS

RESULT 1
US-09-620-312D-617
Sequence 617, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jlan-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 617
LENGTH: 907
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (61)..(747)
US-09-620-312D-617

Query Match 17.3% Score 54.8; DB 4; Length 907;
Best Local Similarity 50.0%; Pred. No. 5.6e-09;
Matches 137; Conservative 0; Mismatches 137; Indels 0; Gaps 0;
DB 4 AAGTGCACACACTGAGAAAGATACCTTCCTTGCATAGAGGTGATGCTGCTA 63
595 AAGGTTCACGTGTTAGAGACCCAGTTCCTTCATCTTGGATATAGAGGTGATGCTGAGACTA 594

QY 6 GGCCTCTCAACCATTAACGCGGCCCATCTGCTGGGGCCAAATTGCATGTCGCTGGAAAC 123
 Db 595 GGTCTTCGACACTGTCCATTAATATGTGTGAGAGGAGGAGGATCAATGATGTGCTGGCAGT 654
 QY 124 TCTATAATTTGGCGCTCGAGCCGAGAGCATCATATGTCGTGAGGAAAGGCGTGAG 183
 Db 655 GCTATTATGAGAGTGAGAGCCCGACGATGTGTGATCAATCTATTAAAGAAAGTTTGCTCA 714
 QY 184 GGCCTTCAGAACAAAACCTGATTTTGGTGTCTCTGTAAAGTACCTCCGCTTTT 243
 Db 715 GAAGCTGCTCAGAAAGTCTCTGTATCGGTAAACATAAGAGCCAGTGTTCCGT 774
 QY 244 TTATTTCGTGCGGTTTGTAGTTCAAAACATGAAGTA 277
 Db 775 CATGAATCTCCCTTTTACTGGAAACAGGAATA 808

```

RESULT 2
US-09-620-312D-618
; Sequence 618, Application US/09620312D
; Patent No. 6559662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Mehrman, Tom
; APPLICANT: Xue, Aiding J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunhui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; FILE REFERENCE: 784C1P2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ. ID NOS: 1105
; SOFTWARE: pt_fl_genes Version 1.0
; SEQ ID NO 618
; LENGTH: 961
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(801)
; US-09-620-312D-618

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	Query Match	17.3%	Score 54.8;	DB 4;	Length 961;
	Best Local Similarity	50.0%;	Pred. No. 5.8e-09;		
	Matches 137/;	Conservative 0;	Mismatches 137/;	Indels 0;	Gaps 0;
QY	4	AAGGTGGCACACATGAGAAAGAACCCCTTCCCTTGACATAGAGGTTGATGTCGTCTTA			63
Db	589	AAGGTTACTGCTGTGAGGACCAGTCCCATCTTTGGATAAGAGGTGATGTCGATGA			648
QY	64	GGTCTCTCAACCATAGACGTGGCCGCATCTGCTGGGGCCATTGATGTCGCTGGAAGC			123
Db	649	GGTCTCAACATGTCCATTAATGTGTCAGAGGACAGAGATTAACATGATGTCTGGGCAGT			708
QY	124	TCATATTTGGCGCTGGCGAACCCAGAGCCATTCATATCTGTCTGAGGAAGAGCGTCAG			183

Db	70	GCATTATAGAGGATGAAAGACCCAGATCTGTGATCAATCATTTATAGAAATGTTTGCTCA	768
Qy	184	GGCTCCGACAAACAAAACATGATTTTGTGGTGTTCGTGCTAAAGTACCTCCGGTTTTT	243
Db	769	GAACTGCTCAGAAACGTTCTCTGTATCGGGAACCATTAAGAGCCAGTGTTCGTIT	828
Qy	244	TTTATTGTCGGCTTTTACGTCAACATGAACCTA	277
Db	829	CATGAATCTCCCTTTTACTGGAAACAGGATA	862

```

RESULT 3
US-09-248-796A-3134
/ Sequence 3134, Application US/09248796A
/ Patent No. 6747137
/ GENERAL INFORMATION:
/ APPLICANT: Keith weinstock et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
/ TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.132
/ CURRENT APPLICATION NUMBER: US/09/248,796A
/ CURRENT FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 60/096,409
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ SEQ ID NO 3134
/ LENGTH: 795
/ TYPE: DNA
/ ORGANISM: Candida albicans
/ US-09-248-796A-3134

```

Query Match	Best Local Similarity	Score	DB 4	Length
Matches	86	Conservative	57	Indels
		Pred. No.	6,1e-08	Gaps
QY	4	AAGGTGGCACTACGAGAAAGAAAGTACCCCTTCCCTTGACATGAGAGTTGATGAGGTCTA	63	
Db	589	AAGGTCAAAACATTAAAGAGAAATATACCCCACTTGAATGTTCAAGTTGATGAGAGATTG	648	
QY	64	GGTCTTCAACCATAGACGTGGCCGCACTTCTGTGGGCCAATTGCATGTCGTGGAAC	123	
Db	649	GGGAGGATCAATTCAACCTGTGCGAGATGCTGTGCATATGATGTGTCGGGACC	708	
QY	124	TCTAATTTGGCGGTGGGACC	146	
Db	709	TGGTGTTTAAACGAGAACCC	731	

```

RESULT 4
US-09-313-294A-3583/C
/ Sequence 3583, Application US/09313294A
/ Patent No. 6476212
/ GENERAL INFORMATION:
/ APPLICANT: Lalgudi, Raghunath V.
/ APPLICANT: Ito, Laura Y.
/ APPLICANT: Sherman, Bradley K.
/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EARS
/ FILE REFERENCE: PL-0017 US
/ CURRENT APPLICATION NUMBER: US/09/313,294A
/ CURRENT FILING DATE: 1999-05-14
/ NUMBER OF SEQ ID NOS: 7600
/ SOFTWARE: PERL Program
/ SEQ ID NO 3583
/ LENGTH: 271
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Inctyle ID No. 6476212 700611933H1
/ NAME/KEY: unsure
/ LOCATION: 244, 259

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OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3583

Query Match 15.9%; Score 50.4; DB 4; Length 271;
Best Local Similarity 78.9%; Pred. No. 1.1e-07;
Matches 71; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

OY 224 AAGTACTCCCTCGCTTTTATTCGCGCTTTAGTCAACATGACTAGCGGAC 283
DB 269 AATATATCCNCATCTTTTATNTGCGGCTTTAGTTGAA-ATGAAGTACGCGGC 211
OY 284 GACTGATTTGAGGATGAGGAGTACTT 313
DB 210 GCGAAATTTGAGAGACAGATGACTT 181

RESULT 5
US-09-691-270A-19/c
Sequence 19, Application US/09691270A
Patent No. 6627795

GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Sean J. Coughlan
TITLE OF INVENTION: CAROTENOID BIOSYNTHESIS ENZYMES
FILE REFERENCE: B1115 US NA2
CURRENT APPLICATION NUMBER: US/09/691,270A
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: 60/083,042
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: PCT/US99/08789
PRIOR FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: MICROSOFT OFFICE 97
SEQ ID NO 19
LENGTH: 1246
TYPE: DNA
ORGANISM: Zea mays

FEATURE:
NAME/KEY: unsure
LOCATION: (367)
OTHER INFORMATION: n = a, c, g or t
US-09-691-270A-19

Query Match 14.6%; Score 46.2; DB 4; Length 1246;
Best Local Similarity 76.0%; Pred. No. 7.9e-06;
Matches 57; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 240 TTTTATTCGCGCTTTAGTCAACATGACTAGCGGCGACTATTCGAGAA 299
DB 1104 TTTTATTCGCGCTTTAGTCAACATGACTAGCGGCGACTATTCGAGAA 1045
OY 300 TGGAGGAGTACTTC 314
DB 1044 CGAGTATCTTTC 1030

RESULT 6
US-09-107-532A-2422
Sequence 2422, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 2422:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

FEATURE:
NAME/KEY: misc.feature
LOCATION: (B) LOCATION 1...663
SEQUENCE DESCRIPTION: SEQ ID NO: 2422:
US-09-107-532A-2422

Query Match 12.0%; Score 38; DB 4; Length 663;
Best Local Similarity 55.2%; Pred. No. 0.0047;
Matches 74; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

OY 15 ACTGAGAAAGAGTACCTTCCCTTGACATGAGGTTGATGCTGCTGCTTCAAC 74
DB 492 ACGTAGAGAGAAATGAGCTTATGCAATCGAAGTAGTGGCGAATGCTTCCAGAAC 551
OY 75 CATGACGCTGGCGGATCTGCTGGGCGCAATGCAATGCTGCTGGAAGCTTATATTGG 134
DB 552 AGCAAAATCTGTAAGATGAGGCGGCGATGCTTCTGTCAGATCATATATCTATCG 611
OY 135 CGCTGGGACCCAG 148
DB 612 AGCCGAAATCCAG 625

RESULT 7
US-09-404-879A-378/c
Sequence 378, Application US/09404879A
Patent No. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 378
LENGTH: 395
TYPE: DNA
ORGANISM: Homo sapiens
US-09-404-879A-378

Query Match 10.9%; Score 34.4; DB 3; Length 395;
Best Local Similarity 63.1%; Pred. No. 0.068;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGCTAGGCTCCTTCAACCATAGACGTGGCCGCAATCTGCTGGGCCAATTGCATGCTGC 116
DB 109 TGGTGCAGGTGCTGCAACAGTAGAGTGGCTGTTCTGCTGCTGATTGGAAACAGTCTT 50

QY 117 TGGAGCTTATATTTGGCGCTGC 140
DB 49 TGGCAGCCTTATCATTTGATATGC 26

RESULT 8

US-09-667-857-378/c
Sequence 378, Application US/09667857
Patent No. 6699664
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Reiter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C5
CURRENT APPLICATION NUMBER: US/09/667,857
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 378
LENGTH: 395
TYPE: DNA
ORGANISM: Homo sapiens
US-09-667-857-378

Query Match 10.9%; Score 34.4; DB 4; Length 395;
Best Local Similarity 63.1%; Pred. No. 0.068;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGCTAGGCTCCTTCAACCATAGACGTGGCCGCAATCTGCTGGGCCAATTGCATGCTGC 116
DB 109 TGGTGCAGGTGCTGCAACAGTAGAGTGGCTGTTCTGCTGCTGATTGGAAACAGTCTT 50

QY 117 TGGAGCTTATATTTGGCGCTGC 140
DB 49 TGGCAGCCTTATCATTTGATATGC 26

RESULT 9

US-09-854-133-314
Sequence 314, Application US/09854133
Patent No. 6759508
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Radoch
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 314
LENGTH: 591

TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(591)
OTHER INFORMATION: n = A,T,C or G
US-09-854-133-314

Query Match 10.9%; Score 34.4; DB 4; Length 591;
Best Local Similarity 63.1%; Pred. No. 0.086;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGCTAGGCTCCTTCAACCATAGACGTGGCCGCAATCTGCTGGGCCAATTGCATGCTGC 116
DB 328 TGGTGCAGGTGCTGCAACAGTAGAGTGGCTGTTCTGCTGCTGATTGGAAACAGTCTT 387

QY 117 TGGAGCTTATATTTGGCGCTGC 140
DB 388 TGGCAGCCTTATCATTTGATATGC 411

RESULT 10

US-09-949-016-22949/c
Sequence 22949, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22949
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-22949

Query Match 10.9%; Score 34.4; DB 4; Length 601;
Best Local Similarity 63.1%; Pred. No. 0.086;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGCTAGGCTCCTTCAACCATAGACGTGGCCGCAATCTGCTGGGCCAATTGCATGCTGC 116
DB 164 TGGTGCAGGTGCTGCAACAGTAGAGTGGCTGTTCTGCTGCTGATTGGAAACAGTCTT 105

QY 117 TGGAGCTTATATTTGGCGCTGC 140
DB 104 TGGCAGCCTTATCATTTGATATGC 81

RESULT 11

US-09-949-016-22950/c
Sequence 22950, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768

;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 22950
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-22950

Query Match
Best Local Similarity 10.9%; Score 34.4; DB 4; Length 601;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGTCTAGGCTCTTAACACCATAGAGTGGCGCCATCTGCTGGGGCCAAATTGATGCTGCG 116
DB 266 TGGTCCAGGTGCTGCAACAGTAGAGTGGCTGTTCTGGTGGTGGATTGGAACAGTCTT 207
QY 117 TGGAGCTCTATATTGCGCGCTGC 140
DB 206 TGGCAGCCTTATCATTTGTTATGC 183

RESULT 12
US-09-949-016-22951/c
;; Sequence 22951, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 22951
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-22951

Query Match

Best Local Similarity 10.9%; Score 34.4; DB 4; Length 601;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGTCTAGGCTCTTAACACCATAGAGTGGCGCCATCTGCTGGGGCCAAATTGATGCTGCG 116
DB 554 TGGTCCAGGTGCTGCAACAGTAGAGTGGCTGTTCTGGTGGTGGATTGGAACAGTCTT 495
QY 117 TGGAGCTCTATATTGCGCGCTGC 140
DB 494 TGGCAGCCTTATCATTTGTTATGC 471

RESULT 13
US-09-949-016-195227/c
;; Sequence 195227, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14

;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 195227
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-195227

Query Match
Best Local Similarity 10.9%; Score 34.4; DB 4; Length 601;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGTCTAGGCTCTTAACACCATAGAGTGGCGCCATCTGCTGGGGCCAAATTGATGCTGCG 116
DB 164 TGGTCCAGGTGCTGCAACAGTAGAGTGGCTGTTCTGGTGGTGGATTGGAACAGTCTT 105
QY 117 TGGAGCTCTATATTGCGCGCTGC 140
DB 104 TGGCAGCCTTATCATTTGTTATGC 81

RESULT 14
US-09-949-016-195228/c
;; Sequence 195228, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 195228
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-195228

Query Match
Best Local Similarity 10.9%; Score 34.4; DB 4; Length 601;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGTCTAGGCTCTTAACACCATAGAGTGGCGCCATCTGCTGGGGCCAAATTGATGCTGCG 116
DB 266 TGGTCCAGGTGCTGCAACAGTAGAGTGGCTGTTCTGGTGGTGGATTGGAACAGTCTT 207
QY 117 TGGAGCTCTATATTGCGCGCTGC 140
DB 206 TGGCAGCCTTATCATTTGTTATGC 183

RESULT 15
US-09-949-016-195229/c
;; Sequence 195229, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

```

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FASTSEQ For Windows Version 4.0
; SEQ ID NO 195229
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-195229

```

```

Query Match      10.9%; Score 34.4; DB 4; Length 601;
Best Local Similarity 63.1%; Pred. No. 0.086;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGTCTAGGCTCTTCAACCATAGACGCGCCGATCTGCTGGGCCAATTGCATCGTCGC 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 554 TGGTGCAGGTGCTGCAACAGTAGAGAGTGGTCTGCTGCTGCTGATGGAAACAGTCTT 495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 117 TGGAGCTCTATATTGGCGCTGC 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 494 TGGCAGCCTTATCATTTGTTATGC 471
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: May 4, 2005, 12:28:07
 Job time : 97.4677 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 113.536 Seconds
(without alignments)
5591.830 Million cell updates/sec

Title: US-09-300-482-298

Perfect score: 388
Sequence: 1 ggagagaagaagaagaatg.....ttaagctggagaccctcgt 388

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155.2	40.0	267	4	US-09-313-294A-2427 Sequence 2427, Ap
2	88.8	22.9	907	4	US-09-620-312D-617 Sequence 617, App
3	88.8	22.9	3556	3	US-09-276-531-8 Sequence 618, App
4	85	21.9	961	4	US-09-620-312D-618 Sequence 618, App
5	83.6	21.5	916	4	US-08-956-171E-1149 Sequence 1149, Ap
6	80.8	20.8	903	4	US-08-781-986A-1149 Sequence 1149, Ap
7	80.8	20.8	993	4	US-09-583-110-947 Sequence 947, App
8	80.8	20.5	663	4	US-09-107-433-453 Sequence 453, App
9	79.4	20.1	690	4	US-09-107-532A-2422 Sequence 2422, Ap
10	77.8	20.1	690	4	US-09-134-000C-1299 Sequence 1299, Ap
11	77.6	20.0	1236025	3	US-08-961-527-149 Sequence 149, App
12	76.4	19.7	1230025	4	US-09-198-452A-1 Sequence 1, Appli
13	76.4	19.7	1230230	4	US-09-513-999C-1817 Sequence 1817, Ap
14	75.8	19.5	434	4	US-09-902-540-9495 Sequence 9495, Ap
15	75.6	19.5	643	4	US-09-902-540-9495 Sequence 1080, Ap
16	75.6	19.5	14101	4	US-09-902-540-1080 Sequence 152, App
17	69	11.8	493	3	US-09-221-017B-2557 Sequence 2557, Ap
18	68.2	11.6	723	4	US-09-543-681A-2557 Sequence 3071, Ap
19	68	17.5	560	4	US-09-710-279-3071 Sequence 1966, Ap
20	68	17.5	645	3	US-09-134-001C-1986 Sequence 3077, Ap
21	68	17.5	672	4	US-09-710-279-3077 Sequence 3513, Ap
22	68	17.5	3008	4	US-09-710-279-3513 Sequence 4257, Ap
23	68	17.5	3246	4	US-09-710-279-4257 Sequence 4240, Ap
24	68	17.3	3276	4	US-09-710-279-4240 Sequence 3134, Ap
25	67	17.3	795	4	US-08-248-796A-3134 Sequence 110, App
26	65.4	16.9	1234	3	US-08-858-207A-110 Sequence 2, Appli
27	60.6	15.6	4403765	3	US-09-103-840A-2

28	60.6	15.6	441529	3	US-09-103-840A-1 Sequence 1, Appli
C 29	58	14.9	1019	3	US-08-714-918-79 Sequence 79, Appl
C 30	58	14.9	1019	3	US-09-265-315-79 Sequence 79, Appl
C 31	58	14.9	1019	3	US-09-265-315-79 Sequence 79, Appl
C 32	58	14.9	1019	3	US-09-266-417-79 Sequence 79, Appl
C 33	58	14.9	1019	4	US-09-528-709-79 Sequence 79, Appl
C 34	58	14.9	1019	4	US-09-527-745-79 Sequence 79, Appl
C 35	56	14.4	705	4	US-09-489-039A-2344 Sequence 2344, Ap
C 36	54.4	14.0	702	4	US-09-328-352-1855 Sequence 1855, Ap
C 37	52.8	13.6	1830121	4	US-09-557-884-1 Sequence 1, Appli
C 38	52.8	13.6	1830121	4	US-09-643-990A-1 Sequence 1, Appli
C 39	51.8	13.4	410	4	US-09-513-999C-1816 Sequence 1816, Ap
C 40	51.4	13.2	1664976	4	US-08-916-421B-1 Sequence 1, Appli
41	51.4	13.2	1664976	4	US-09-592-002-31 Sequence 31, Appli
42	48.8	12.6	65792	4	US-09-596-002-31 Sequence 31, Appli
C 43	47	12.1	640681	4	US-09-790-988-1 Sequence 1, Appli
C 44	46	11.9	693	4	US-09-252-991A-825 Sequence 825, App
45	42.2	10.9	696	4	US-09-489-039A-2525 Sequence 2525, Ap

ALIGNMENTS

RESULT 1
US-09-313-294A-2427
Sequence 2427, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Ialqudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 2427
LENGTH: 267
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700552657H1
US-09-313-294A-2427

Query Match 40.0%; Score 155.2; DB 4; Length 267;
Best Local Similarity 75.4%; Pred. No. 1.5e-42;
Matches 193; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY	116	GCTCCATGACATCATGATGGGCAATTTGTCCTCCCAATTAATTAATGCGCTCCACT	175
DB	1	GCTACATATGACATCATGATGGGCACTGCTCTCAACGACTATATGGGCTCCGCT	60
QY	176	TATTGAAGTTGAGAAAGACACAAAGCATTTTGGATGTCACCTTATGTTACAAA	235
DB	61	GATTCAGAGCTTGAGAAACATCCAAAGCATATTTGACATGCTTATGTCACAAA	120
QY	226	TCCCTTGATTAATGTTGAACCTTGCAAAAGCTGGTGTCTGCTTTACATTCACGT	295
DB	121	GCTTCAGATTTACGTAAGAACATTTGGAAGGCTGGCTTCTGATTCACATTCATAT	180
QY	296	AGAGACATCAAAAGTAATCTGGAAAGAACTTATCCAAAGATCAAGTCACATGATGAT	355
DB	181	AGAACTGCTGAGACAACTGGCAAGATCTATCCAAAGCATTAATCAAAAGGTATGCG	240
QY	356	TCTTGCTGATGATTA 371	
DB	241	GCTGTGATGATCATGA 256	

RESULT 2
US-09-620-312D-617

Sequence 617, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aiding J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhilwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: Polypeptides
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PC_FL_genes Version 1.0
SEQ ID NO 617
LENGTH: 907
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (61)..(747)
US-09-620-312D-617

Query Match 22.9%; Score 88.8; DB 4; Length 907;
Best Local Similarity 56.9%; Pred. No. 1,2e-19;
Matches 206; Conservative 0; Mismatches 147; Indels 9; Gaps 2;
QY 33 AAAATAGCTCTTCGATGCTCTTCGACCTTCGCAATTTGGCTTCGAGGCTCAGGC 92
DB 76 AAGATTGGCCCGTCATCTCAACAGCGACCTGGCCATTGAGGGCCGAGTCTCCGG 135
QY 93 ATGCTCCACTTGGGCGCGATGGCTCCACATGACATCATGATGGGCAATTTGTCCC 152
DB 136 ATGCTAGACTGCGGGCGGATGATGACCTGACCTGAATGACGGGCAATTTGTCCC 195
QY 153 AATTAACTAATGGGCTCCAGTATTTGAAGTTGAAGAAAGCA-----CACAAAGCA 206
DB 196 AACATCACCTTTGGTACCCCTGTGTAGAAAGCTTCGAAAGCGTAAAGCCAGACCCCT 255
QY 207 TATTTGATGTGACCTTATGTTAAATCCTCTTGAATTAATTTGAACCTTGGCAAAA 266
DB 256 TTTCTTGAACATGACATGATGTGTCCAAAGCAGAAAGTGGTAAAGCCATAGCTGTA 315
QY 267 GCTGTGCTTCGGTTTAACTTACAGTACGTAAGACATCAAAAGATTAAGTGAAGAACTT 326
DB 316 GCAGAGGCAATCAATACACCTTTCATCTCGAG--GCTACTGAGAACCCAGGGGCTTTG 372
QY 327 ATCCAAAGATCAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 386
DB 373 ATTTAAAGCATTCGAGGAGATGGATGAAGTGGCTTGGCCATCAACAGAACTCA 432
QY 387 GT 388
DB 433 GT 434

RESULT 3
US-09-276-531-8
Sequence 8, Application US/09276531
Patent No. 618968
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LIVERPOOL
CLONE: 1753826
US-09-276-531-8
Query Match 22.9%; Score 88.8; DB 3; Length 356;
Best Local Similarity 56.9%; Pred. No. 2.7e-19;
Matches 206; Conservative 0; Mismatches 147; Indels 9; Gaps 2;
QY 33 AAAATAGCTCTTCGATGCTCTTCGACCTTCGCAATTTGGCTTCGAGGCTCAGGC 92
DB 72 AAGATTGGCCCGTCATCTCAACAGCGACCTGGCCATTGAGGGCCGAGTCTCCGG 131
QY 93 ATGCTCCACTTGGGCGCGATGGCTCCACATGACATCATGATGGGCAATTTGTCCC 152
DB 132 ATGCTAGACTTGGGCGGATGATGACCTGACCTGAATGACGGGCAATTTGTCCC 191
QY 153 AATTAACTAATGGGCTCCAGTATTTGAAGTTGAAGAAAGCA-----CACAAAGCA 206
DB 192 AACATCACCTTTGGTACCCCTGTGTAGAAAGCTTCGAAAGAGTAAAGCCAGACCCCT 251
QY 207 TATTTGATGTGACCTTATGTTAAATCCTCTTGAATTAATTTGAACCTTGGCAAAA 266
DB 252 TTTCTTGAACATGACATGATGTGTCCAAAGCAGAAAGTGGTAAAGCCATAGCTGTA 311

QY 267 GCTGTCCTTCTGTTTACATTCAGTACATCAAGATACTGAAAGACTT 326
 DB 312 GAGGAGCCAAATCAGTACCTTTCTCTGAG--GCTACTGAGAACCCAGGGCTTTG 368
 QY 327 ATCCAAAGATCAAGTACATGATGATTCCTGCTGATGATCAATTAAGCTGAGACCCC 386
 DB 369 ATTAAGACATTCGGAGATGAGATGAGATGAGTGGCTTCCATCAACAGGAACTCTA 428

QY 387 GT 388
 DB 429 GT 430

RESULT 4
 US-09-620-312D-618
 ; Sequence 618, Application US/09620312D
 ; Patent No. 6569662
 ; GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod
 APPLICANT: Zhang, Jie
 APPLICANT: Ren, Feiyun
 APPLICANT: Chen, Rui-hong
 APPLICANT: Zhao, Qing A.
 APPLICANT: Wehrman, Tom
 APPLICANT: Xue, Aidong J.
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yundong
 APPLICANT: Wang, Dunrui
 APPLICANT: Wang, Zhiwei
 APPLICANT: John Tillinghast
 APPLICANT: Drmanac, Radoje T.
 TITLE OF INVENTION: No. 656962e1 Nucleic Acids and
 TITLE OF INVENTION: Polypeptides
 FILE REFERENCE: 784CIP2B
 CURRENT APPLICATION NUMBER: US/09/620,312D
 FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1105
 SOFTWARE: pt_FL_genes Version 1.0
 SEQ ID NO 618
 LENGTH: 961
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (61)..(801)
 US-09-620-312D-618

Query Match 21.9%; Score 85; DB 4; Length 961;
 Best Local Similarity 59.6%; Pred. No. 2.4e-18;
 Matches 164; Conservative 0; Mismatches 105; Indels 6; Gaps 1;

QY 33 AAAATAGCTCTTCGATGCTCTCTTCGCACTTCGCCAATTTGGCTTCGAGGCTGACGCC 92
 DB 76 AAGATTGGCCCGTCCTCTCTCAACAGACCTGGCCAAATTTAGGGCGAGTCCCTCCG 135
 QY 93 ATGCTCCACTTCGCGCCGATGCTCCACATGACATGATGGGATTTTGTCC 152
 DB 136 ATGCTAGACTCTGGGGCCATTAATCTGACCTGAGATGAGACGGCATTTTGTCC 195
 QY 153 AATTACTATTGGCGCTCCAGTTATTTGAAGTTGAGAAAGCA-----CACAAAGCA 206
 DB 196 AACATACACTTTGGTCACTCTGGTGAAGAGCTTCGAAAGCAGTACGAGCCCT 255
 QY 207 TATTGATTCGACCTTATGTTAACAATCTCTGATTTATGTTAACCCTTGGCAAA 266

DB 256 TTCTTGACATGACATGATGCTGTCGAAGCCAGAACAGTGGTAAAGCAATGCTGTA 315
 QY 267 GCTGTCCTTCTGTTTACATTTACAGTAGAC 301
 DB 316 GCAGAGCCAAATCAGTACACCTTTCATCTCGAGGC 350

RESULT 5
 US-08-956-171E-1149/c
 ; Sequence 1149, Application US/08956171E
 ; Patent No. 6593114
 ; GENERAL INFORMATION:
 APPLICANT: Charles Kunach
 Gil H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5256
 CORRESPONDENCE ADDRESS:
 ADDRESS: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/956,171E
 FILING DATE: 20-Oct-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/009,861
 FILING DATE: January 5, 1996
 APPLICATION NUMBER: 08/791,986
 FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
 NAME: Mark J. Hyman
 REGISTRATION NUMBER: 46,789
 REFERENCE/DOCKET NUMBER: PB248P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (240) 314-1224
 TELEFAX: (301) 309-8439
 INFORMATION FOR SEQ ID NO: 1149:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 916 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1149:
 US-08-956-171E-1149

Query Match 21.5%; Score 83.6; DB 4; Length 916;
 Best Local Similarity 53.6%; Pred. No. 7.1e-18;
 Matches 192; Conservative 2; Mismatches 161; Indels 3; Gaps 1;

QY 31 CCAAAATAGCTCTTCGATGCTCTCTTCGCACTTCGCCAATTTGGCTTCGAGGCTCAGC 90
 DB 745 CAAATATATCATCATATTAATATCTGTTGATTTTGGATTACAAACATTAATAAC 686
 QY 91 GATGCTCACTTGGCGCGGATGCTCCACATGACATGATGAGGCAATTTGTCC 150
 DB 685 GACTGAAGACAGCGCGTGAAGATTCATTTGATGATGATGATGATGATGATGATGATG 626
 QY 151 CCAATTAATCTTTGGCGCTCCAGTTATTTGAAGTTGAGAAAGCAACAAAGGATATT 210
 DB 625 CTAATATATCTATTTGTTACCAATTTAGATGACGTAAGAAAGCAACAAATTAACCTA 566

QY	21	TGAGTGTGACCTTAGTGTACAAATCCTCTGATTAGTTAGAACCTTGGCAAAAGCTG	270
Db	565	TAGACGTACATTTGAGTATGAAAAATCCGAAAGAAATATATGATTCATTTCACAAACATG	506
QY	271	GTCCTTCGTGTTTATCATTTCAAGTACATCAATCAAAAAGATTAATCGAAGAACTTATCC	330
Db	505	GTGCCATATGATTTCAATTCATGCGA---ATCAACGCCATCAATTCATCATGTCGTATTC	449
QY	331	AAAGAAATCAAGTCATCGCATGATTCCTGCTGTGACATTTAAAGCGTGGAGCCCCGT	388
Db	448	AAATGATTTAAACATTTAGATTAATAAAAGCTGGGTGTATTTAAATCTTGATACGCCAT	391

```

1  RESULT 6
2  US-08-781-986A-1149/C
3  Sequence 1149, Application US/08781986A
4  Patent No. 6737248
5  GENERAL INFORMATION:
6  APPLICANT: Charles Kunach
7  TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
8  NUMBER OF SEQUENCES: 5355
9  CORRESPONDENCE ADDRESS:
10 ADDRESSSEE: Human Genome Sciences, Inc.
11 STREET: 9410 Key West Avenue
12 CITY: Rockville
13 STATE: Maryland
14 COUNTRY: USA
15 ZIP: 20850
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
18 COMPUTER: HP Vectra 486/33
19 OPERATING SYSTEM: MSDOS version 6.2
20 SOFTWARE: ASCII Text
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/781,986A
23 FILING DATE:
24 CLASSIFICATION: 435
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:
27 FILING DATE:
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Benson, Bob
30 REGISTRATION NUMBER: 30,446
31 REFERENCE/DOCKET NUMBER: PB248PP
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (301) 309-8504
34 TELEFAX: (301) 309-8512
35 INFORMATION FOR SEQ ID NO: 1149:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 916 base pairs
38 TYPE: nucleic acid
39 STRANDEDNESS: double
40 TOPOLOGY: linear
41 US-08-781-986A-1149

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Query Match	21.5%	Score 83.6;	DB 4;	Length 916;
Best Local Similarity	53.6%;	Pred. No. 7,1e-18;		
Matches 199;	Conservative 2;	Mismatches 161;	Indels 3;	Gaps 1.
QY	31	CGAAATAAGCTCCCTCGATGCTCTCTTCGACCTTGGCCCAATTTGGCTTCGAGGCTCAGC	90	
Db	745	CAAACTAATATCCATCACTTATTATCTGTGTGATTTTGGATTTCACATGATTTAAAC	686	
QY	91	GCAATGCTCACTTGGGCGCCGATTTGGCTCCACATGACATATGATGGGCAATTTGGCC	150	
Db	685	GACTTGAAGAAGCAGCGCGTCGACCGAGATCTATTTTGATGTTATGGATGGTCAATTTGGC	626	
QY	151	CCAAATTAACATATGGGCGCTCCAACTTATTGGAATTTGAGGAAGACACAAAGCATATT	210	
Db	625	CTAATATATCTATTTGTTTACCATATTTAGTCAGCTAAGAAAGGACCAACATTAACCTA	566	
QY	211	TGGATTGTCACTTATGGTTACAAATCTCTTGAATTAATGTTGAAACCTTGGCAAAAGCTG	270	

Db	565	TAGACGTACATTGANTGATTGAAATCCAGAAAATATTATTCATCATTTTGCGAACAATG	506
Oy	271	GTGCTTCGTGGTTTTACATTTCCACGTAGACATCAAAAAGATACTGAAAGAACTTATCC	330
Db	505	GTGCGCATATGATTTCAATTATCTATCGCA--ATCAACGCCATATTCATCTGTGCTATTTC	449
Oy	331	AAAGATCAAGTCACATGCGCATGATTCCTGTGTACGATTTAAAGCTGGGACCCCGGT	388
Db	448	AAATGATTAAACATTTAAGTATAAAAGAGCTGGGTGTAGTATTAATCTCGGTACCCCAT	391

```

RESULT 7
US-09-583-110-947
; Sequence 947 Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 947
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-947

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Query Match	20.8%	Score 80.8	DB 4	Length 903
Best Local Similarity	53.7%	Pred. No. 6.3e-17		
Matches 191	Conservative 0	Mismatches 162	Indels 3	Gaps 1
QY	33	AAAATAGCTCCCTGCATGCTCTCTCTCCAGCTATGGCCAAATTGGCTTCGGAGGCTCAGGCG	92	
Db	259	AAGATTGCTCCGTCAATTCTGGCAGCAGATTATGGCAACTTTGAACGTGAANAACGT	318	
QY	93	ATGCTCCACTTGGCGCCGATGGCTCCACATGACATCATGATGGGCAATTTGTCCCC	152	
Db	319	CTAGAGCAACTGGGGGAGAAATATGGCCATATGCATATACAGACAGTCATTTTGTACCG	378	
QY	153	AATTAACTATTGGCGCTCCCACTGATTGAAGTTTGAGAAAGCACACAAAGCATATTGG	212	
Db	379	CAATACGTTTGGTGGCAGGTGTGTGAGAGCCCTTGCTCTCATATGAATGATGGTTTC	438	
QY	213	GATTGTCACTTATGTTACAAATCTCTTGATATGTTGAACCTTGGCAAAAGCTGT	272	
Db	439	GATTGCCACTGATGGTGTCAAAACCTGAGCATATCTGGAAAGATTTTGGCGCTGACGT	498	
QY	273	GCTTCTGGTTTACATTCACTTCAGTGAAGACATCAAAAGATTAACGTGAAGAAGAACTTATCA	332	
Db	499	GCAGACATCATCAGTATTCATGTAGA--AGCAACACCTCATATTCAATGGCGCCCTCCA	555	
QY	333	AGATTCAAAGTCACATGGCAGATGATTCCTGGGTGACATTAAGCCTGGAGACCCCGT	388	
Db	556	AAATTTGCTTACCTGGAGTTAAGCCTTACGTGTATATCAATCTCTGGCACACACGT	611	

RESULT 8
 US-09-107-433-453
 : Sequence 453: Application US/09107433
 : Parent No. 66800744
 : GENERAL INFORMATION:
 : APPLICANT: Lynn A Doucette-Stamm and David Bush
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
 : SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
 : THERAPEUTICS FOR DIAGNOSIS

NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 453:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...993
SEQUENCE DESCRIPTION: SEQ ID NO: 453:
US-09-107-433-453
Query Match 20.8%; Score 80.8; DB 4; Length 993;
Best Local Similarity 53.7%; Pred. No. 6,7e-17;
Matches 191; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

33 AAAATAGCTCTTCATGCTCTTCCTCCGACTTCGCAATTTGGCTTCGAGGCTCAGCGC 92
349 AAGATTGCTCCGTCATTTCTGGCAGAGATTAATGCAATTTGAACGTAATCAAAAGT 408
93 ATGCTCCACTTGGGGCCGATTTGGCTCCATGACATGATATGATGGGATTTTGTCCCC 152
409 CTAGAAGCAATCGGGGCAAAATATGCGCATATGATATGATGACAGTATTTTGTACCG 468
153 AATTTAACTATTGGCGCTCCAGTATTGAAAGTTGAGAAAGACACAAGGATATTG 212
469 CAAATCAGTTTGGTGCAGGTGTGTCGAGAGCTTCGTCCTCATATGTAAGATGTTTC 528
213 GATTTACCTTATGTTTAAATCTCTTGAATATGTAACCTTTGGCAAAAGCTGT 272
529 GATTCGCACTTATGTTTCAAACTCTGAGCATCATCTGGAAGATTTTGGCGTGAAGT 588
273 GCTTCGTTTACATTTACGATGAGATCAAAAGATTAATCTGGAAGAAATTAACCA 332
589 GAGACATCATATGATATGATGAGA--AGCAACCTCATATTCATGCGCGCTCCAA 645
333 AGAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 388
646 AAAATTCGTTCACTCGAGTAAAGCTTCACTGATGATGATGATGATGATGATGATG 701

RESULT 9
US-09-107-532A-2422
Sequence 2422, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2422:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...663
SEQUENCE DESCRIPTION: SEQ ID NO: 2422:
US-09-107-532A-2422
Query Match 20.5%; Score 79.4; DB 4; Length 663;
Best Local Similarity 52.8%; Pred. No. 1.6e-16;
Matches 195; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

20 GGAATGACACGAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 79
3 GGAATGACACGAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 62
80 CGAGCTCAGCGCATGCTCCTCCTGATGCTCTTCCTCCGACTTCGCAATTTGGCTTC 139
63 AGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 122
140 GATTTTGTCCCAATTTAATTTGATGATGATGATGATGATGATGATGATGATGATG 199
123 CCAATTTTGTCCCAATTTAATTTGATGATGATGATGATGATGATGATGATGATGATG 182
200 AAGGATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 259
183 TAAATTCAGCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 242

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QY 260 GGCAAAAGTGTGCTTCTGTTTACATTTCAGCTAGACATCAAAAGATAACTGGAA 319
    |||
Db 243 TGCAAAAGCTGAGAGATATCATCTACTGTCACGCTCGAAGCACTCTCTCATATTCATCG 302
QY 320 AGAAGCTTATCCAAAGATCAAGTACATGAGCATGATTTCTGTGTAGATTAAGCTGG 379
    |||
Db 303 GGCACTT---CAATGACAAAAGAGTTAGAGTTAAAGCTGAGTAGTATCAATCCAGG 359
QY 380 GACCCCGCT 388
    |||
Db 360 AACACCACT 368
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RESULT 10

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US-09-134-000C-1299
; Sequence 1299, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lym Doucelte-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1299
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1299
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Query Match 20.1%; Score 77.8; DB 4; Length 690;
Best Local Similarity 52.3%; Pred. No. 5.7e-16;

Matches 197; Conservative 0; Mismatches 177; Indels 3; Gaps 1;

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QY 9 AAGAAAGATGGGAATGACACCGAAATAGCTCTTCGATGCTCTTCGACTTCGCC 68
    |||
Db 16 AATATTAAGGAGCGAGCCAAATGAACTAGACCACTTTCATAGTCCGATTTTGGC 75
QY 69 AATTGGCTTCGAGGCTAGGCGCATGCTCCACTTCGCGCGCATTTGGCTCCATGAC 128
    |||
Db 76 AATTGAAAGAGATATCCGTTAGTAGAAGATTTAGAGACAGATTATTCATGTGAT 135
QY 129 ATCATGATGGGCAATTTTGCCCAATTAACTATTGGGCTCCAGTTTGAAGTTG 188
    |||
Db 136 GTCATGAGCGGTCAATTTTGCCCAATTAACTATTGGGCGAATATGCTTACCGATT 195
QY 189 AGAAAGCACAAAGGCAATTTGATGTCACCTTATGTTACAATCTCTGATTAT 248
    |||
Db 196 CGTTCAGTACAAAATCTACCATTTGATGTTCAATTGATGATTAACACTGAAATTAAT 255
QY 249 GTTGAACCTTGGCAAAAGCTGCTCTTCGTTTAACTTTACGTTGAGACATCAAAA 308
    |||
Db 256 ATCATGCTTTTCCGAAGCCGCTGCGATTTATTACCTTCACGAAGAAACACCC 315
QY 309 GATTAAGTGAAGAACTTATCCAAAGATCAAGTACATGAGCATGATTCGTGTGACGA 368
    |||
Db 316 CATAT---TTCAATCGTCTTCAATGATTTAAATGCGGGGTGTAAGCTGGGCTAAC 372
QY 369 TTAAGCCTGGGAGCCG 385
    |||
Db 373 ATCAATCTGGGACACC 389
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RESULT 11

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US-08-961-527-149
; Sequence 149, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
```

```
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 1256 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-149
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Query Match 20.0%; Score 77.6; DB 3; Length 1256;
Best Local Similarity 53.1%; Pred. No. 3.7e-15;

Matches 189; Conservative 0; Mismatches 164; Indels 3; Gaps 1;

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QY 33 AAAATAGCTCTTGATGCTCTCTCCGACTTCGCCAATTTGGCTTCGAGCTCAGCCG 92
    |||
Db 4786 AAGATTGCTCGTAATTTCTGGCAGCAGATTATGCAACTTTGAACGTGAATCAACGT 4845
QY 93 ATGCTCACTTGGCGCGCATTTGCTTCACATGACATCATGATGGGCAATTTGTCCC 152
    |||
Db 4846 CTAGAACCACTGGGGCAGAAATATGCCATATGATATCATGACAGTCAATTTGTACCG 4905
QY 153 AATTAACTTTGGCGCTCCAGTATTGAAAGTTTGAAGAAAGCACAAAGCATATTTG 212
    |||
Db 4906 CAAATCGTTTGGTGAAGGTGTGTGAGAGGCTTCCTCATGTATGTAAGATGTTTC 4965
QY 213 GATTGACCTTATGTTTAAATCTCTTGATTATGTTGAACCTTGGCAAAAGCTGTG 272
    |||
Db 4966 GATTCACCTTGAATGTTGTAAGCCTGAGCATCATCTGAAAGATTTTGGCTGAGGT 5025
QY 273 GCTTGTGTTTACATTTTACGTTAGACATCAAAAGATPACTGAAAGAACTTATCAA 332
    |||
Db 5026 GCAGACATCATCGTATTCATGTAGA---AGCAACCCCTCATATTCATGCGCCCTCAA 5082
QY 333 AGAATCAAGTCACATGATTTCTGTGTAGCATTTAAAGCTGGGAGCCCGCT 388
    |||
Db 5083 AAAATTCGTTCACTGGAGTTAAAGCTTACGTGCTTATCAATCTGGCAGATCACT 5138
```

RESULT 12

```
US-09-198-452A-1/C
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
```


TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
FILE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc.feature
LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc.feature
LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc.feature
LOCATION: (45001)..(60000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc.feature
LOCATION: (300001)..(315000)

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NAME/KEY: misc.feature
LOCATION: (315001)..(330000)
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LOCATION: (330001)..(345000)
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NAME/KEY: misc.feature
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LOCATION: (405001)..(420000)
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LOCATION: (615001)..(630000)
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LOCATION: (630001)..(645000)
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LOCATION: (645001)..(660000)
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NAME/KEY: misc.feature
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OTHER INFORMATION: n=a or c or g or t

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/ LOCATION: (675001)..(690000)
/ OTHER INFORMATION: n=a or c or g or t
/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: n=a or c or g or t
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/ LOCATION: (765001)..(780000)
/ OTHER INFORMATION: n=a or c or g or t
/ NAME/KEY: misc_feature
/ LOCATION: (780001)..(795000)
/ OTHER INFORMATION: n=a or c or g or t
/ NAME/KEY: misc_feature
/ LOCATION: (795001)..(810000)
/ OTHER INFORMATION: n=a or c or g or t
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/ LOCATION: (810001)..(825000)
/ OTHER INFORMATION: n=a or c or g or t
/ NAME/KEY: misc_feature
/ LOCATION: (825001)..(840000)
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/ NAME/KEY: misc_feature
/ LOCATION: (840001)..(855000)
/ OTHER INFORMATION: n=a or c or g or t
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/ LOCATION: (855001)..(870000)
/ OTHER INFORMATION: n=a or c or g or t
/ NAME/KEY: misc_feature
/ LOCATION: (870001)..(885000)
/ OTHER INFORMATION: n=a or c or g or t
/ NAME/KEY: misc_feature
/ LOCATION: (885001)..(900000)
/ OTHER INFORMATION: n=a or c or g or t
/ NAME/KEY: misc_feature
/ LOCATION: (900001)..(915000)
/ OTHER INFORMATION: n=a or c or g or t
/ NAME/KEY: misc_feature
/ NAME/KEY: misc_feature

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Query Match      19.7%; Score 76.4; DB 4; Length 1230025;
Best Local Similarity 54.7%; Pred. No. 1.4e-13;
Matches 152; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

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QY 35 AATAGCTCTTCGATGCTCTCTTCGACTTGGCAATTGGCTTCGAGGCTCAGCCGAT 94
DB 232716 AGTGGCCCTTGATTAAGGGGAGATCTTACCTGTTGGGTGAGAGCAAAAAAACT 232657
QY 95 GCTCATTGCGCGCCGATTTGGCTCCACATGACATGATGAGGCAATTTTGTCCCAA 154
DB 232656 AGAGAGCGCGGAGATGATTTTATACATGATGATGATGAGGCACTTTGTTCCGAA 232597
QY 155 TTTAACCTTTGGCGCTCAGTTATTTGAAGTTTGAAGACACACAAAGGATATTGGA 214
DB 232596 CCTTACTTTTGGTCCAGGATCATTTGCTCCATTAATGATCTACGGATCTTATTTTGA 232537
QY 215 TTGTCACTTATGTTACAAATCCTTTGATTATTTGAACCTTGGCAAAAGCTGTGC 274
DB 232536 AGTCACCGCTATGATTTACATCTTTTGAATTTAAGAAAGTTTCTGTCGTGTC 232477
QY 275 TTCTGTTTACATTTACGATGAGACATCAAAAGATA 312
DB 232476 GGATGAAATTTATGATACCTTTGAAGCTTCAGAGGATA 232439

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RESULT 13
US-09-438-185A-1/c
/ Sequence 1, Application US/09438185A
/ Patent No. 6822071
/ GENERAL INFORMATION:
/ APPLICANT: Stephens, Richard
/ APPLICANT: Mitchell, Wayne
/ APPLICANT: Kalman, Sue
/ APPLICANT: Davis, Ronald
/ TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
/ FILE REFERENCE: 018941-000411US
/ CURRENT APPLICATION NUMBER: US/09/438,185A
/ PRIOR APPLICATION NUMBER: US 60/108,279
/ PRIOR FILING DATE: 1998-11-12
/ PRIOR APPLICATION NUMBER: US 60/128,606
/ PRIOR FILING DATE: 1999-04-08
/ NUMBER OF SEQ ID NOS: 1074
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 1230230
/ TYPE: DNA
/ ORGANISM: Chlamydia pneumoniae
US-09-438-185A-1

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Query Match      19.7%; Score 76.4; DB 4; Length 1230230;
Best Local Similarity 54.7%; Pred. No. 1.4e-13;
Matches 152; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

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```

QY 35 AATAGCTCTTCGATGCTCTCTTCGACTTGGCAATTGGCTTCGAGGCTCAGCCGAT 94
DB 222428 AGTGGCCCTTGATTAAGGGGAGATCTTACCTGTTGGGTGAGAGCAAAAAAACT 222369
QY 95 GCTCATTGCGCGCCGATTTGGCTCCACATGACATGATGAGGCAATTTTGTCCCAA 154
DB 222368 AGAGAGCGCGGAGATGATTTTATACATGATGATGATGAGGCACTTTGTTCCGAA 222309
QY 155 TTTAACCTTTGGCGCTCAGTTATTTGAAGTTTGAAGACACACAAAGGATATTGGA 214
DB 222308 CCTTACTTTTGGTCCAGGATCATTTGCTCCATTAATGATCTTATTTTGA 222249
QY 215 TTGTCACTTATGTTACAAATCCTTTGATTATTTGAACCTTGGCAAAAGCTGTGC 274
DB 222248 AGTCACCGCTATGATTTACATCTTTTGAATTTAAGAAAGTTTCTGTCGTGTC 222189
QY 275 TTCTGTTTACATTTACGATGAGACATCAAAAGATA 312
DB 222188 GGATGAAATTTATGATACCTTTGAAGCTTCAGAGGATA 222151

```

```

RESULT 14
US-09-513-999C-1817
/ Sequence 1817, Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclert, A.Y.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ PATENT NO. 6783961
/ FILE REFERENCE: 59.US2.REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 1817
/ LENGTH: 434
/ TYPE: DNA

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1 ORGANISM: Homo sapiens
2 FEATURE:
3 NAME/KEY: CDS
4 LOCATION: 105..434
5 FEATURE:
6 NAME/KEY: misc_feature
7 LOCATION: 12
8 OTHER INFORMATION: y=c or t
9 FEATURE:
10 NAME/KEY: misc_feature
11 LOCATION: 13
12 OTHER INFORMATION: y=c or t
13 FEATURE:
14 NAME/KEY: misc_feature
15 LOCATION: 28
16 OTHER INFORMATION: y=c or t
17 FEATURE:
18 NAME/KEY: misc_feature
19 LOCATION: 86
20 OTHER INFORMATION: k=g or t
21 FEATURE:
22 NAME/KEY: misc_feature
23 LOCATION: 117
24 OTHER INFORMATION: k=g or t
25 FEATURE:
26 NAME/KEY: misc_feature
27 LOCATION: 290
28 OTHER INFORMATION: w=a or t
29 FEATURE:
30 NAME/KEY: misc_feature
31 LOCATION: 291
32 OTHER INFORMATION: n=a, g, c or t
33 FEATURE:
34 NAME/KEY: misc_feature
35 LOCATION: 292
36 OTHER INFORMATION: n=a, g, c or t
37 FEATURE:
38 NAME/KEY: misc_feature
39 LOCATION: 293
40 OTHER INFORMATION: n=a, g, c or t
41 FEATURE:
42 NAME/KEY: misc_feature
43 LOCATION: 317
44 OTHER INFORMATION: n=a, g, c or t
45 FEATURE:
46 NAME/KEY: UNSURE
47 LOCATION: 5
48 OTHER INFORMATION: Xaa=Gly or Trp
49 FEATURE:
50 NAME/KEY: UNSURE
51 LOCATION: 63
52 OTHER INFORMATION: Xaa=any one of the twenty amino acids
53 FEATURE:
54 NAME/KEY: UNSURE
55 LOCATION: 71
56 OTHER INFORMATION: Xaa=Asp or Glu
57 ;
58 ;
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	Query Match	19.5%	Score 75.8	DB 4	Length 434
	Best Local Similarity	55.4%	Pred. No. 2.1e-15		
	Matches 201	Conservative 3	Mismatches 143	Indels 10	Gaps 3
QY	33	AAATAGCTCCTTGATGATCTCTCTTCCACATTCGGCAATTTGGTTCGAG-GCTCAGCG	91		
Db	44	AAGATTGGCCCGTCATCTCTCAACAGCACTGGGCAATTTAKGGGGCGAAGTCTCCGG	103		
QY	92	CATGCTCACTTCGGCGCCGATTTGGCTCAACATGACATCATGATGGGCAATTTGTGCC	151		
Db	104	GATCTCTAGACTCTCTKGGGCCGATTAATCTCACCTGACCTAATGACGGGCAATTTGTGCC	163		
QY	152	CAATTTAATATTGGCGCTCCAGTATTGAAGATTGAGAAAGCA-----CACAAAGGC	205		
Db	164	CAACATACCTTTGGTTCACCCCTGTGGTGAAGAAAGCCTTGAAAAGCACTAAGGCGACAGACC	223		

QY 206 ATATTGGATTGTACCTTAAGTGTAACAATCCCTTGATTATGTTAAACCTTGGCAA 265
 Db 224 TTCTTTGACATGCACATGATGTGTCTCCAAACCAGAACATGGGTAAAGCAATGGCTGT 283
 QY 266 AGCTGTGCTCTGTGGTTTAACTTTCACGTAGAGACATCAAAAAGTAACTGGAAAGACT 325
 Db 284 AGCAGGMMNNNAATCAGTACACCTTCACTCTG---AGCTACTAGAACCCAGAGGGGCTT 340
 QY 326 TATCCAAAGAATCAACGTCAATGCGATATTCCTGTGTGTGCAATTAAAGCTGGGACCCC 385
 Db 341 GATTAAAGACATTTGGGAGAAATGGATGAAGCTTGGCTTGCATCAAAACCGAGAACCTC 400
 QY 386 CGT 388
 Db 401 AGT 403

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RESULT 15
US-09-902-540-9495
; Sequence 9495, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9495
; LENGTH: 643
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-9495

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Query Match	19.5%	Score 75.6	DB 4	Length 643
Best Local Similarity	55.3%	Pred. No. 3e-15		
Matches 147	Conservative 0	Mismatches 119	Indels 0	Gaps 0
QY	36	ATAGCTCTTGAGATGCTCTTCTCCGACTCTCCCAATTGTGCGTCCGAGGCTCAGCGCATG	95	
DB	4	ATCTCTCTTGCTTTTGTGTCTGTGACTTGGCGCGCTTGGCGGAAGAGTGCGGCATC	63	
QY	96	CTCCACTTGGCGCGCATTTGGCTCCACATGACATCATGATGGGCATTTTGTGCCAAT	155	
DB	64	GAAACCGCTGGTGCGGATTTGGATTCAAGTGATGATCATGATGAGCGCTTTGTGCCAATC	123	
QY	156	TTAACTATTGGCGCTCCAGTTATTGAAAGTTTGGAAGAACACACAAAGGCATTTTGGAT	215	
DB	124	ATCAGCATTTGGCCCGGTGTGTGTGAGAGCCATCAAGCGGCTGGCGACCAAGCCCTTGGAC	183	
QY	216	TGTACCTTATGTGTTCACAAATCCCTCTTGATTAATGTGAACCCCTGGCAAAAGCTGTCT	275	
DB	184	GTGACCTGTAGATTGTGGAGCCCGAAGCGCTAAGTGAGGAGCTTGTGAAGCGGGGGCG	243	
QY	276	TCTGGTTTTCATTCACTTCAGTGAAGAC	301	
DB	244	GACGTGCTGACGGTGCAAGTGAAGAC	269	

Search completed: May 4, 2005, 12:28:18
Job time : 124.536 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 440.206 Seconds
(without alignments)
5365.716 Million cell updates/sec

Title: US-09-300-482-298

Perfect score: 388

Sequence: 1 ggagagaagaagaagaatg.....ttaagcctggagcccccgt 388

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:*

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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	388	100.0	417	11	US-09-987-899-4761
2	370	95.4	837	17	US-10-424-599-109667
3	358.4	92.4	845	17	US-10-424-599-109666
4	261.6	67.4	629	18	US-10-021-323-6163
5	252.2	65.0	266	11	US-09-987-899-4727
6	250.4	64.5	272	11	US-09-987-899-4725
7	247	63.7	499	18	US-10-425-115-92527
8	241.8	62.3	260	11	US-09-987-899-4726
9	239.8	61.8	1406	18	US-10-437-963-45062
10	225.4	58.1	1026	18	US-10-767-701-12139
11	223.8	57.7	1027	17	US-10-425-114-4370

12	223.8	57.7	1250	18	US-10-425-115-155395	Sequence 155395, A
13	219.6	56.6	959	17	US-10-425-114-28690	Sequence 28690, A
14	215.6	55.6	705	17	US-10-393-840-519	Sequence 519, App
15	215	55.4	508	17	US-10-393-840-513	Sequence 513, App
16	213.4	55.0	459	17	US-10-393-840-520	Sequence 520, App
17	211.6	54.5	410	17	US-10-393-840-521	Sequence 521, App
18	208	53.6	502	17	US-10-393-840-514	Sequence 514, App
19	205.8	53.0	228	11	US-09-987-899-4728	Sequence 4728, App
20	202.8	52.3	415	11	US-09-987-899-4723	Sequence 4723, App
21	184.2	47.5	668	18	US-10-425-115-41147	Sequence 41147, A
22	173.8	44.8	363	17	US-10-424-599-11379	Sequence 11379, A
23	165.4	42.6	280	9	US-09-923-876-4114	Sequence 4114, App
24	165.4	42.6	280	10	US-09-923-876-4114	Sequence 4114, App
25	161.8	41.7	269	11	US-09-987-899-4706	Sequence 4706, App
26	159.4	41.1	557	18	US-10-425-115-180354	Sequence 180354, A
27	159.4	41.1	557	18	US-10-425-115-180354	Sequence 180354, A
28	134	34.5	438	17	US-10-424-599-112304	Sequence 112304, A
29	115.6	29.8	791	18	US-10-425-115-155373	Sequence 155373, A
30	108.8	28.0	606	18	US-10-021-323-7334	Sequence 7334, App
31	103.6	26.7	229	11	US-09-987-899-4705	Sequence 4705, App
32	99.4	25.6	193	17	US-10-424-599-43914	Sequence 43914, A
33	91.4	23.6	319630	17	US-10-398-221-7	Sequence 7, Appl
34	91.4	23.6	3011208	17	US-10-398-221-2058	Sequence 2058, App
35	88.8	22.9	730	17	US-10-092-900A-321	Sequence 321, App
36	88.8	22.9	907	15	US-10-037-270-617	Sequence 617, App
37	88.8	22.9	907	17	US-10-117-722-617	Sequence 617, App
38	88.8	22.9	1205	18	US-10-729-473-12	Sequence 12, Appl
39	88.8	22.9	4397	18	US-10-357-930-25186	Sequence 25186, A
40	88.8	22.9	4397	18	US-10-357-930-25186	Sequence 25186, A
41	87.2	22.5	876	17	US-10-092-900A-319	Sequence 319, App
42	85	21.9	961	15	US-10-037-270-618	Sequence 618, App
43	85	21.9	961	17	US-10-117-722-618	Sequence 618, App
44	83.6	21.5	916	8	US-08-781-986A-1149	Sequence 1149, App
45	83.6	21.5	916	17	US-10-329-624-1149	Sequence 1149, App

ALIGNMENTS

RESULT 1

US-09-987-899-4761

Sequence 4761, Application US/09987899

Publication No. US20040116682A1

GENERAL INFORMATION:

APPLICANT: Celix, Nordine

APPLICANT: Liu, Jindong

APPLICANT: Miller, Phillip W.

APPLICANT: O Connell, Keith M.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

TITLE OF INVENTION: With the Carbon Assimilation Pathway

FILE REFERENCE: 16517.258

CURRENT APPLICATION NUMBER: US/09/987,899

CURRENT FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: US 09/262,979

PRIOR FILING DATE: 1999-03-04

PRIOR APPLICATION NUMBER: US 60/076,712

PRIOR FILING DATE: 1998-03-06

NUMBER OF SEQ ID NOS: 7341

SEQ ID NO 4761

LENGTH: 417

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: LIB3040-057-Q1-B1-C5

US-09-987-899-4761

Query Match

Best Local Similarity

Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 388; DB 11; Length 417;

100.0%; Pred. No. 2.76-110;

1 GGAGGAAGAAGAAGAATGGAATGACACCGAATAGCTCTTCGATGCTCTTCGCG 60

30 GGAGGAAGAAGAAGAATGGAATGACACCGAATAGCTCTTCGATGCTCTTCGCG 89

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OY 61 ACTTGCCAAATTTGGCTTCCTCCAGGCTCAGCGCATCTTCACCTTGGCGCCGATTTGGCTCC 120
Db 90 ACTTGCCAAATTTGGCTTCCTCCAGGCTCAGCGCATCTTCACCTTGGCGCCGATTTGGCTCC 149
OY 121 ACATGACATCATGATGGGCAATTTTGTCCCAATTTACATATTTGGGCTCCAGTTATTTG 180
Db 150 ACATGACATCATGATGGGCAATTTTGTCCCAATTTACATATTTGGGCTCCAGTTATTTG 209
OY 181 AAAGTTGAGAAAGACACAAAGGCATTTTGGATTTGTACCTTATGTTTCAAAATCTTC 240
Db 210 AAAGTTGAGAAAGACACAAAGGCATTTTGGATTTGTACCTTATGTTTCAAAATCTTC 269
OY 241 TTGATTTATTTGTAACCTTGGCAAAAGCTGTGCTTCTGTTTACATTTTACGTAGAGA 300
Db 270 TTGATTTATTTGTAACCTTGGCAAAAGCTGTGCTTCTGTTTACATTTTACGTAGAGA 329
OY 301 CATCAAAAGATTAAGCTGGAAGAACTTATCCAAAGATTCAGTCATGCGATGATTCCTG 360
Db 330 CATCAAAAGATTAAGCTGGAAGAACTTATCCAAAGATTCAGTCATGCGATGATTCCTG 389
OY 361 GTGTAGCATTAAGCTCGGAGACCCCGCT 388
Db 390 GTGTAGCATTAAGCTCGGAGACCCCGCT 417
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RESULT 2

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US-10-424-599-109667
; Sequence 109667, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 109667
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_70042C.1
US-10-424-599-109667
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Query Match Best Local Similarity 95.4%; Score 370; DB 17; Length 837; Pred. No. 1.6e-104;

Matches 376; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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OY 3 AGAAGAAAGAAAGATGGGATGACACCGAAATAGCTCCTTGATGCTCTCTCCGAC 62
Db 22 AGAAGAAAGAAAGATGGGATGACACCGAAATAGCTCCTTGATGCTCTCTCCGAC 81
OY 63 TTCGCCAATTTGGCTTCGAGGCTCAGCGCATGCTCCACTTGGGCGCGATTTGGCTCCAC 122
Db 82 TTCGCCAATTTGGCTTCGAGGCTCAGCGCATGCTCCACTTGGGCGCGATTTGGCTCCAC 141
OY 123 ATGACATCATGATGGGCAATTTGTCCCAATTTAATATTTGGGCTCCGATTTATGAA 182
Db 142 ATGACATCATGATGGGCAATTTGTCCCAATTTAATATTTGGGCTCCGATTTATGAA 201
OY 183 AGTTGAGAAAGACACAAAGGCATTTTGGATTTGTCACTTATGTTTACAAATCTCTT 242
Db 202 AGTTGAGAAAGACACAAAGGCATTTTGGATTTGTCACTTATGTTTACAAATCTCTT 261
OY 243 GATTATGTTGAACCTTGGCAAAAGCTGTGCTTCTGTTTATATTTTCACTGATAGACA 302
Db 262 GATTATGTTGAACCTTGGCAAAAGCTGTGCTTCTGTTTATATTTTCACTGATAGACA 321
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OY 303 TCAAAAGATATCGGAAGAACTTATCCAAAGATCAAGTCATGCGATGATTCCTGT 362
Db 322 TCAAAAGATATCGGAAGAACTTATCCAAAGATCAAGTCATGCGATGATTCCTGT 381
OY 363 GTAGCATTTAAAGCTCGGAGACCCCGCT 388
Db 382 GTAGCATTTAAAGCTCGGAGACCCCGAT 407
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RESULT 3

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US-10-424-599-109666
; Sequence 109666, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 109666
; LENGTH: 845
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_70041C.1
US-10-424-599-109666
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Query Match Best Local Similarity 92.4%; Score 358.4; DB 17; Length 845; Pred. No. 6.7e-101;

Matches 365; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Db 59 AGAAGAAAGAAAGATGGGATGACACCGAAATAGCTCCTTGATGCTCTCTCCGAC 118
OY 63 TTCGCCAATTTGGCTTCGAGGCTCAGCGCATGCTCCACTTGGGCGCGATTTGGCTCCAC 122
Db 119 TTCGCCAATTTGGCTTCGAGGCTCAGCGCATGCTCCACTTGGGCGCGATTTGGCTCCAC 178
OY 123 ATGACATCATGATGGGCAATTTGTCCCAATTTAATATTTGGGCTCCGATTTATGAA 182
Db 179 ATGACATCATGATGGGCAATTTGTCCCAATTTAATATTTGGGCTCCGATTTATGAA 238
OY 183 AGTTGAGAAAGACACAAAGGCATTTTGGATTTGTCACTTATGTTTACAAATCTCTT 242
Db 239 AGTTGAGAAAGACACAAAGGCATTTTGGATTTGTCACTTATGTTTACAAATCTCTT 298
OY 243 GATTATGTTGAACCTTGGCAAAAGCTGTGCTTCTGTTTATATTTTCACTGATAGACA 302
Db 299 GATTATGTTGAACCTTGGCAAAAGCTGTGCTTCTGTTTATATTTTCACTGATAGACA 358
OY 303 TCAAAAGATTAAGCTGGAAGAACTTATCCAAAGATCAAGTCATGCGATGATTCCTGT 362
Db 359 TCAAAAGATTAAGCTGGAAGAACTTATCCAAAGATCAAGTCATGCGATGATTCCTGT 418
OY 363 GTAGCATTTAAAGCTCG 378
Db 419 GTAGCATTTAAAGCTCG 434
```

RESULT 4

```
US-10-021-323-6163
; Sequence 6163, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
```

APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021.323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 6163
LENGTH: 629
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
OTHER INFORMATION: Clone ID: LIB3828-016-Q1-K6-B2
US-10-021-323-6163

Query Match 67.4%; Score 261.6; DB 18; Length 629;
Best Local Similarity 81.5%; Pred. No. 8.9e-71;
Matches 303; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 14 AAAGATGGGAATGACACCGAAAATAGCTCTTGATGCTCTTCCGACTTCCCAATT 73
DB 92 AAAGATGGGTGAACACCAAAATATGCTTCATCCATGCTTTCATGCGATTTTGTAACTT 151
QY 74 GGCTTCGAGGCTGACGGCAGTCTCCACTTGGCGCCGATTTGGCTCCACATGACATCAT 133
DB 152 AGCATCAAGGCAAGGCAAGCTGCTGAGCTGAGCTGATGCTTCAATGGAATATCAT 211
QY 134 GGATGGGCAATTTTGTCCCAATTTAACTATTGGCCCTCCAGTTATTTGAAAGTTGAGAAA 193
DB 212 GGATGGGCAATTTTGTCCCAATTTAACTATTGGCCCTCCAGTTATTTGAAAGTTGAGAAA 271
QY 194 GCACACAAAGCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 253
DB 272 GCACACAAAGCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 331
QY 254 ACCCTTGGCAAAAGCTGTGCTTCTGCTTTTCACTTTCACGTAAGACATCAAAAGATTA 313
DB 332 ACTTTTGGTAAAGTGTGCTTCTGCTTTTCACTTTCACGTAAGACATCAAAAGATTA 391
QY 314 CTGGAAGAAGCTTATCCAAAGATCAAGTCAATGATGATTTCTGCTGATGATTTAA 373
DB 392 CTGGAAGAAGCTTATCCAAAGATCAAGTCAATGATGATTTCTGCTGATGATTTAA 451
QY 374 GCCTGGGACCCC 385
DB 452 GCCTGGGACACC 463

RESULT 5
US-09-987-899-4727
Sequence 4727, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordin
APPLICANT: Liu, Jingdong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: With the Carbon Assimilation Pathway
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987, 899
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262, 979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076, 712
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4727
LENGTH: 266
TYPE: DNA
ORGANISM: Glycine max

FEATURE:
OTHER INFORMATION: Clone ID: 70100767H1
US-09-987-899-4727

Query Match 65.0%; Score 252.2; DB 11; Length 266;
Best Local Similarity 97.0%; Pred. No. 4.8e-68;
Matches 257; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 10 AAGAAAAGATGGGAATGACACCGAAAATAGCTCTTCGATGCTCTTCCGACTTCCGCA 69
DB 2 AAGAAAAGATGGGAATGACACCGAAAATAGCTCTTCGATGCTCTTCCGACTTCCGCA 61
QY 70 ATTGGCTTCCGAGGCTGAGGCAATGCTCCACTTGGCGGATTTGGCTCCACATGACCA 129
DB 62 ATTGGCTTCCGAGGCTGAGGCAATGCTCCACTTGGCGGATTTGGCTCCACATGACCA 121
QY 130 TCATGATGGGCAATTTTGTCCCAATTTAACTATTGGGCTCCAGTTATTTGAAAGTTTGA 189
DB 122 TCATGATGGGCAATTTTGTCCCAATTTAACTATTGGGCTCCAGTTATTTGAAAGTTTGA 181
QY 190 GAAAGCACAAAGGCAATTTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 249
DB 182 GAAAGCACAAAGGCAATTTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 241
QY 250 TTGAACCTTGGCAAAAGCTGGTC 274
DB 242 TTGAACCTTGGCAAAAGCTGGTC 266

RESULT 6
US-09-987-899-4725
Sequence 4725, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordin
APPLICANT: Liu, Jingdong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: With the Carbon Assimilation Pathway
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987, 899
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262, 979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076, 712
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4725
LENGTH: 272
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(272)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 700971857H1
US-09-987-899-4725

Query Match 64.5%; Score 250.4; DB 11; Length 272;
Best Local Similarity 96.9%; Pred. No. 1.8e-67;
Matches 254; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 AAGAAAAGATGGGAATGACACCGAAAATAGCTCTTCGATGCTCTTCCGACTTCCGCA 62
DB 11 AAGAAAAGATGGGAATGACACCGAAAATAGCTCTTCGATGCTCTTCCGACTTCCGCA 70
QY 63 TTGGCAATTTGGCTTCCGAGGCTGAGGCAATGCTCCACTTGGCGGATTTGGCTCCAC 122
DB 71 TTGGCAATTTGGCTTCCGAGGCTGAGGCAATGCTCCACTTGGCGGATTTGGCTCCAC 130
QY 123 ATGACATGATGATGGGCAATTTTGTCCCAATTTAACTATTGGGCTCCAGTTATTTGAA 182

Db 131 ATGACATCANTGATGGGCAATTTGTCCCAATTTAACTATGCGCTCCAGTTATTGAA 190
QY 183 AGTTTGAAAACACACAAAGGCAATTTGGATTTGCACTTATGTTAGTAAATCTCTT 242
Db 191 AGTTTGAAAAGCACAAAGGATATTGGATTGTCACTTATGTTAGTAAATCTCTT 250
QY 243 GATTATGTTGAACCTTGGGCAA 264
Db 251 GATTATGTTGAGNCTTGGCAA 272

RESULT 7

US-10-425-115-92527
; Sequence 92527, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 92527
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_184377C.1
US-10-425-115-92527

Query Match 63.7%; Score 247; DB 18; Length 499;
Best Local Similarity 78.7%; Pred. No. 2.8e-66;

Matches 225; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 14 AAGATGGGATGACACCGAAATAGCTCTTCGATGCTCTTCGCACTTGGCAATTT 73
Db 90 AACCATGGCGGCGGCGGCGAGATAGCGCGTCAATGCTCTGTGGACTTGGCAACCT 149
QY 74 GCTTCGAGGCGTCAAGCGATGCTCACTTGGCGCGGATTTGGCTCCAGTGAATCAT 133
Db 150 CCGCTCGAGGCGGCGAGCGATGCTCGCGCGCGCGCATGGCTCCAGTGAATCAT 209
QY 134 GGATGGGCAATTTTGTCCCAATTTAACTATGCGCTCCAGTTATGAAAGTTGAGAA 193
Db 210 GGATGGGCACTTCGTTCCCAATTTAACTATGAGACTCCAGTATGAGAGCTTGAAGAA 269
QY 194 GCACCAAAAGGATTTGGATTTGACCTTATGTTGTTAAATCTCTTGAATTTGTTGA 253
Db 270 GCACCAAAAGGATTTGGAATGCTGCACTGATGTTGCAAAATCTCTTGAATTTGTTGA 329
QY 254 ACCCTTGGCAAAAGCTGTGCTTCTGTTTCAATTTACGTAAGAGATCAAAAGATTA 313
Db 330 GGCATTGGAAAAGCTGTGCTTCTGATTTCAATTTCAATTAAGAAAGTGAAGAGATTA 389
QY 314 CTGGAAGAAGCTTATCCAAAGATCACTGATGCTGATTTCTGGTTAGCAATTTAA 373
Db 390 CTGGAAGAAGCTCAACCAAGATCACTGATGCTGATTTCTGGTTAGCAATTTAA 449
QY 374 GCGTGGGAGCCCGCT 388
Db 450 GCTGTGTAATCTCTGT 464

RESULT 8

US-09-387-899-4726
; Sequence 4726, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordin

; APPLICANT: Lau, Jindong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O'Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 4726
; LENGTH: 260
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701064495H1
US-09-987-899-4726

Query Match 62.3%; Score 241.8; DB 11; Length 260;
Best Local Similarity 97.2%; Pred. No. 8.3e-65;
Matches 246; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 AGAAAGAAAGAAAGATGGAATGACACCGAAATAGCTCTTCGATGCTCTTCCGAC 62
Db 8 AGACAGAAAGAAAGATGGAATGACACCGAAATAGCTCTTCGATGCTCTTCCGAC 67
QY 63 TTCCGCAATTTGGCTTCGAGAGCTCAAGGCAATGCTCCACTTGGCGCGGATTTGGCTCCAC 122
Db 68 TTCCGCAATTTGGCTTCGAGAGCTCAAGGCAATGCTCCACTTGGCGCGGATTTGGCTCCAC 127
QY 123 ATGACATCATGATGGGCAATTTGTCCCAATTTAACTATGCGCTCCAGTATTTGAA 182
Db 128 ATGACATCATGATGGGCAATTTGTCCCAATTTAACTATGCGCTCCAGTATTTGAA 187
QY 183 AGTTTGAAAACACACAAAGGATTTGGATTTGATGCTGATTTGTTAAATCTCTT 242
Db 188 AGTTTGAAAACACACAAAGGATTTGGATTTGATGCTGATTTGTTAAATCTCTT 247
QY 243 GATTATGTTGAC 255
Db 248 GATTATGTTGAC 260

RESULT 9

US-10-437-963-45062
; Sequence 45062, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barabazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 45062
; LENGTH: 1406
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1406)
; OTHER INFORMATION: unsure at all n locations

FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_48063C.1
US-10-437-963-45062

Query Match
Best Local Similarity 61.8%; Score 239.8; DB 18; Length 1406;
Matches 286; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

DB 26 GACACCGAATAAGCTCTTCGATGCTCTCTTCGACCTTCGCAATTGGCTTCGAGGC 85
DB 70 GCGGCGAAGATAGCCCGCTCGATGCTCTCTTCGACCTTCGCAATTGGCTTCGAGGC 129
QY 86 TGAGCGCATGCTCCCATCTTCGCGCGCATTCGCTCCCATGACATATGATGAGGATTT 145
DB 130 CGACCGCATGCTCCCGCTTCGCGCGCATTCGCTCCCATGACATATGATGAGGATTT 189
QY 146 TGTCCCATTTAACTATTGGCGCTCCAGTTATTTGAAGTTGAGAAACACACAAAGGC 205
DB 190 TGTCTCTATCTTACTATTGGAGCTTCATGATTCAGACTTCGAGAACACACCAAGGC 249
QY 206 ATATTGGATTGTCACTTATGTTACAAATCTCTTATGTTGAACCTTGGCAAA 265
DB 250 ATATTGGACTCCACTTATGTTGACCAATCTCTGATTTGTAACCAATTAGCAAA 309
QY 266 AGCTGGCTTCTGCTTACATTCACGTAGACATCAAAAGATTAATCTGAAAAGT 325
DB 310 AGCTGGCTTCTGCTTACATTCACGTAGACATCAAAAGATTAATCTGAAAAGT 369
QY 326 TATCCAAAGATCAAGTCAATGACATGATTCCTGCTGATGATTAAGCTGGACCCC 385
DB 370 CATCCAAAGATCAAGTCAATGACATGATTCCTGCTGATGATTAAGCTGGACCCC 429
QY 386 CGT 388
DB 430 TGT 432

RESULT 10
US-10-767-701-12139
Sequence 12139, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 12139
LENGTH: 1026
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAV03-ClUS13660_1
US-10-767-701-12139

Query Match
Best Local Similarity 58.1%; Score 225.4; DB 18; Length 1026;
Matches 277; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

DB 26 GACACCGAATAAGCTCTTCGATGCTCTCTTCGACCTTCGCAATTGGCTTCGAGGC 85
DB 141 GCGGCGAAGATAGCCCGCTCGATGCTCTCTTCGACCTTCGCAATTGGCTTCGAGGC 200
QY 86 TGAGCGCATGCTCCCATCTTCGCGCGCATTCGCTCCCATGACATATGATGAGGATTT 145
DB 201 TGAGCGCATGCTCCCGCTTCGCGCGCATTCGCTCCCATGACATATGATGAGGATTT 260
QY 146 TGTCCCATTTAACTATTGGCGCTCCAGTTATTTGAAGTTGAGAAACACCAAAAGGC 205

DB 261 TGTCTCTATCTGACTATTGGGGCTCCGCTGATTCAGAGCTTGAGAAACATACCAAGC 320
QY 206 ATATTGGATTGTCACTTATGTTACAAATCTCTTATGTTGAACCTTGGCAAA 265
DB 321 ATATTGGACTCCACTTATGTTACAAACCTTACAGTTATGTAAGAACCAATTGGAAA 380
QY 266 AGCTGGCTTCTGCTTACATTCACGTAGACATCAAAAGATTAATCTGAAAAGT 325
DB 381 GCTGGCTTCTGCTTACATTCACGTAGACATCAAAAGATTAATCTGAAAAGT 440
QY 326 TATCCAAAGATCAAGTCAATGACATGATTCCTGCTGATGATTAAGCTGGACCCC 385
DB 441 CATCCAAAGATTAATCAAAAGGATATGCGGCTGTGTATGATGAGGCCAGTACACC 500
QY 386 CGT 388
DB 501 AGT 503

RESULT 11
US-10-425-114-4370
Sequence 4370, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 4370
LENGTH: 1027
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700355680_FLI
US-10-425-114-4370

Query Match
Best Local Similarity 57.7%; Score 223.8; DB 17; Length 1027;
Matches 276; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 26 GACACCGAATAAGCTCTTCGATGCTCTCTTCGACCTTCGCAATTGGCTTCGAGGC 85
DB 172 GCGGCGAAGATAGCCCGCTCGATGCTCTCTTCGACCTTCGCAATTGGCTTCGAGGC 231
QY 86 TGAGCGCATGCTCCCATCTTCGCGCGCATTCGCTCCCATGACATATGATGAGGATTT 145
DB 232 TGAGCGCATGCTCCCGCTTCGCGCGCATTCGCTCCCATGACATATGATGAGGATTT 291
QY 146 TGTCCCATTTAACTATTGGCGCTCCAGTTATTTGAAGTTGAGAAACACCAAAAGGC 205
DB 292 GCTTCTCTATCTTACTATTGGGGCTCCGCTGATTCAGAGCTTGAGAAACATACCAAGC 351
QY 206 ATATTGGATTGTCACTTATGTTACAAATCTCTTATGTTGAACCTTGGCAAA 265
DB 352 ATATTGGACTCCACTTATGTTACAAAGCTTCAAGTTACGTAGAACCAATTGGAAA 411
QY 266 AGCTGGCTTCTGCTTACATTCACGTAGACATCAAAAGATTAATCTGAAAAGT 325
DB 412 GCTGGCTTCTGCTTACATTCACGTAGACATCAAAAGATTAATCTGAAAAGT 471
QY 326 TATCCAAAGATCAAGTCAATGACATGATTCCTGCTGATGATTAAGCTGGACCCC 385
DB 472 CATCCAAAGATTAATCAAAAGGATATGCGGCTGTGTATGATGAGGCCAGTACACC 531
QY 386 CGT 388

Db 532 AGT 534

RESULT 12

US-10-425-115-155395
; Sequence 155395, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 155395
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MR14577_7329C.1
US-10-425-115-155395

Query Match 57.7%; Score 223.8; DB 18; Length 1250;
Best Local Similarity 76.0%; Pred. No. 86-59;

Matches 276; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 26 GACACCGAATAATAGCTCTTCGATGCTCTCTCGAATTGCGCAATTGGCTTCGAGGC 85
Db 189 GGGGGGGAAGATAGCCCGCGATGCTCTCGATGCTTCGCACTTGGCAACTGGCTTCGAGGC 248
QY 86 TCAGCGCATGCTCCATCTGGGCGCGATGCTTCGCACTGAGCATATGATGGGCATTT 145
Db 249 TGAGCGCATGCTCCGCTGAGCGCGCATGCTTCGCACTGAGCATATGATGGGCATTT 308
QY 146 TGTCCCAATTTAATCTATTGGCGCTCCAGTATTGAAAGTTGAGAAAGCACAAGAGC 205
Db 309 CGTTCCTAAGCTGATGATTTGGGGCTCGGATCCAGACTTGGAGAAACATACCAAGC 368
QY 206 AATATTGGATGTCACCTTATGTTCAAAATCTCTTGAATGTTGAACCTTGGCAAA 265
Db 369 AATATTGGATGTCACCTTATGTTCAAAATCTCTTGAATGTTGAACCTTGGCAAA 428
QY 266 AGCTGCTCTCTGCTTTTACATTTCACTAGAGCATCAAAAGATTAAGTGAAGACT 325
Db 429 GGCTGGCGCTTCTGATTCACATTCATATAGAGTTGTTAGAGCACTGGCAAGATCT 488
QY 326 TATCCAAAGATCAAGTCACTGAGCATGATGTTCTGGTGAATTAAGCTGGAGCC 385
Db 489 CATCCAAAGCATTAATCAAAAGGATATGCGGCTGGTGAATTAAGCTGGAGCC 548
QY 386 CGT 388
Db 549 AGT 551

RESULT 13

US-10-425-114-28690
; Sequence 28690, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 28690
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4762-037-D5_FLI
US-10-425-114-28690

Query Match 56.6%; Score 219.6; DB 17; Length 959;
Best Local Similarity 76.3%; Pred. No. 146-57;

Matches 270; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 26 GACACCGAATAATAGCTCTTCGATGCTCTCTCGAATTGCGCAATTGGCTTCGAGGC 85
Db 126 GGGGGGGAAGATAGCCCGCGATGCTCTCGATGCTTCGCACTTGGCAACTGGCTTCGAGGC 185
QY 86 TCAGCGCATGCTCCATCTGGGCGCGATGCTTCGCACTGAGCATATGATGGGCATTT 145
Db 186 TGAGCGCATGCTCCGCTGAGCGCGCATGCTTCGCACTGAGCATATGATGGGCATTT 245
QY 146 TGTCCCAATTTAATCTATTGGCGCTCCAGTATTGAAAGTTGAGAAAGCACAAGAGC 205
Db 246 CGTTCCTAAGCTGATGATTTGGGGCTCGGATCCAGACTTGGAGAAACATACCAAGC 305
QY 206 AATATTGGATGTCACCTTATGTTCAAAATCTCTTGAATGTTGAACCTTGGCAAA 265
Db 306 AATATTGGATGTCACCTTATGTTCAAAATCTCTTGAATGTTGAACCTTGGCAAA 365
QY 266 AGCTGCTCTCTGCTTTTACATTTCACTAGAGCATCAAAAGATTAAGTGAAGACT 325
Db 366 GGGTGGCGCTTCTGATTCACATTCATATAGAGTTGTTAGAGCACTGGCAAGATCT 425
QY 326 TATCCAAAGATCAAGTCACTGAGCATGATGTTCTGGTGAATTAAGCTGG 379
Db 426 CATCCAAAGCATTAATCAAAAGGATATGCGGCTGGTGAATTAAGCTGG 479

RESULT 14

US-10-393-840-519
; Sequence 519, Application US/10393840
; Publication No. US20030229922A1
; GENERAL INFORMATION:
; APPLICANT: Blockberg, Leonard N.
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1012c3
; CURRENT APPLICATION NUMBER: US/10/393,840
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 09/636,800
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/170,862
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 60/148,426
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT NZ/99/00169
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 956
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 519
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-393-840-519

Query Match 55.6%; Score 215.6; DB 17; Length 705;
Best Local Similarity 73.5%; Pred. No. 2,1e-56;

Matches 275; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 9 AAGAAAGATGGAATGACACCGAATAATAGCTCTTCGATGCTCTTCGCACTTGGCC 68

Db 132 AACACAGAGAGGGGTTATCCCTTAATATGCTCCGTCATGTGTCATCAAGACTTTGGC 191
QY 69 AATTGGCTTCGAGGCTCAGGCATGCTCCACTTGGGCGGATTTGGCTCCACATGAC 128
Db 192 AATCTGGCTTCAGAGGCGAAATATATAGCGAAATGTCAGATTTGGTTCATATGAC 251
QY 129 ATCATGATGGGCTTTTGTCCCCAATTTAATATTTGGGCTTCAGTTATGAAAGTTTG 188
Db 252 ATCATGATGGGCTTTTGTCCAAATCTTACCATTTGAGAGCACTGTGATTCAGAGTTTG 311
QY 189 AGAAAGCACACAAGGCTATTTGATGTCACCTTATGTTACAAATCTCTTGATTTAT 248
Db 312 AGGAAGCATACCCAGGCTATTTGATGTCATCTTATGTCACAAACCTCTTGATTTAT 371
QY 249 GTTGAACCTTGGCAAAAGCTGCTGCTTGTGTTTACATTTTCACGTAGACATCAAAA 308
Db 372 GTGAGGCCATTTGCAAAAGCTGAGGCTTCAGGCTTCATTTTCATGTGAGGCTGCCAA 431
QY 309 GATTAATGGAAGAACTTATCCAAAGATCAAGTCATGCGATGATTTCTGTGTGCA 368
Db 432 GACCAATTTGGCAAGATCTCATCAAAAGATCAGAAATGCTGATGCGGCTGAGTGCA 491
QY 369 TTAAGCCTGGGAC 382
Db 492 GTGAAGCTTGAAC 505

RESULT 15
US-10-393-840-513
; Sequence 513, Application US/10393840
; Publication No. US2003022922A1
; GENERAL INFORMATION:
; APPLICANT: Blockberg, Leonard N.
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1012c3
; CURRENT APPLICATION NUMBER: US/10/393,840
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 09/636,800
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/170,862
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 60/148,426
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT NZ/99/00169
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 956
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-393-840-513

Query Match 55.4%; Score 215; DB 17; Length 508;
Best Local Similarity 73.3%; Pred. No. 2.7e-56;
Matches 275; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
QY 8 GAAAGAAAAGTGGGAATGACACCGAAATAGCTCTTGATGCTCTTCCGACTTGGC 67
Db 97 GAACACAGAGAGAGGGGTATATCCCTTAATATGCTCCGTCATGTGTCATCAAGACTTTGC 156
QY 68 CAATTGGCTTCGAGGCTCAGGCTCAGGCTCCACTTGGGCGGATTTGGCTCCACATGGA 127
Db 157 GAATCGGCTTCAGAGGCGAAATATATGACGAAATGTCAGATTTGGTGTATGGA 216
QY 128 CATCATGATGGGCTTTTGTCCCAATTTAATATTTGCGCTCCAGTTATGAAAGTTT 187
Db 217 CATCATGATGGGCTTTTGTCCCAATTTAATATTTGAGAGCACTGTGATTCAGAGTTT 276
QY 188 GAGAAAGCACAAAGGCTATTTGATGTCACCTTATGTTACAAATCCTCTTGATTA 247

Db 277 GAGGAAGCATACCAGGCAATCTTGATTTGTCATCTTAATGTCACAAACCTCTTGATTA 336
QY 248 TGTGAACCTTTGGCAAAAGCTGTGCTTGTGCTTTTACATTTCACTGAGACATCAAA 307
Db 337 TGTGAGCCATTTGCAAAAGCTGAGGCTTCAGGGTTCACTTTTCATGTGAGAGGCTGCCAA 396
QY 308 AGATACTGGAAGAAGAACTTATCCAAAGATCAAGTCACATGCGATGATTCCTGTGTAGC 367
Db 397 AGACATTTGGCAAGATCTCATCAAAAGATCAGAAATGCTGAGGCTGAGAGTGCC 456
QY 368 ATTAAGCCTGGGAC 382
Db 457 AGTGAAGCTTGAAC 471

Search completed: May 4, 2005, 21:11:40
Job time : 443.206 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 80.1777 Seconds
(without alignments)
5591.830 Million cell updates/sec

Title: US-09-300-482-311

Perfect score: 274
Sequence: 1 cttaatcccttcctccacac.....gccaaagcatgcgcgtgacgcg 274

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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2: /cgn2_6/prodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
4: /cgn2_6/prodata/1/ina/5B_COMB.seq: *
5: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
6: /cgn2_6/prodata/1/ina/5B_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46.6	17.0	741	4	US-09-583-110-44
2	46.4	16.9	1288	1	US-08-440-856A-9
3	44.6	16.3	77536	4	US-09-410-551B-1
4	44.6	16.3	77536	4	US-09-940-316B-1
5	44.6	16.3	4403765	3	US-09-103-840A-2
6	44.6	16.3	4411529	3	US-09-103-840A-2
7	43	15.7	701	3	US-09-133-321-1
8	43	15.7	753	4	US-09-252-991A-13584
9	43	15.7	765	4	US-09-252-991A-13860
10	43	15.7	4411529	3	US-09-103-840A-1
11	42.8	15.6	2225	4	US-09-902-540-8186
12	42.8	15.6	6301	4	US-09-902-540-8186
13	42.2	15.4	1187	1	US-08-440-856A-2
14	42	15.3	813	4	US-09-252-991A-6615
15	42	15.3	1029	4	US-09-252-991A-6683
16	42	15.3	1974	4	US-09-252-991A-6585
17	42	15.3	2106	4	US-09-252-991A-6717
18	41.8	15.3	833	2	US-08-403-852D-3
19	41.8	15.3	833	3	US-08-510-646B-3
20	41.8	15.3	833	3	US-09-231-818-3
21	41.8	15.3	833	4	US-09-635-359B-3
22	41.8	15.3	882	4	US-08-818-112-138
23	41.8	15.3	882	3	US-08-818-111-138
24	41.8	15.3	882	3	US-09-056-556-138
25	41.8	15.3	882	3	US-09-072-596-133
26	41.8	15.3	882	4	US-09-252-991A-5644
27	41.8	15.3	882	4	US-09-072-596-138

28	41.8	15.3	1020	4	US-09-252-991A-5550	Sequence 5550, Ap
29	41.8	15.3	2079	2	US-09-252-991A-5584	Sequence 5584, Ap
30	41.8	15.3	5392	2	US-08-403-852D-1	Sequence 1, Appl
31	41.8	15.3	5392	3	US-08-510-646B-1	Sequence 1, Appl
32	41.8	15.3	5392	3	US-09-231-818-1	Sequence 1, Appl
33	41.8	15.3	5392	4	US-09-635-359B-1	Sequence 1, Appl
34	41.6	15.2	290	3	US-08-818-112-37	Sequence 37, Appl
35	41.6	15.2	290	3	US-08-818-111-37	Sequence 37, Appl
36	41.6	15.2	290	3	US-09-056-556-37	Sequence 37, Appl
37	41.6	15.2	290	3	US-09-072-596-37	Sequence 37, Appl
38	41.6	15.2	290	4	US-09-072-596-37	Sequence 37, Appl
39	41.6	15.2	1929	3	US-09-380-420C-1	Sequence 1, Appl
40	41.6	15.2	1929	4	US-09-899-642A-1	Sequence 1, Appl
41	41.4	15.1	490	4	US-10-101-464A-286	Sequence 286, App
42	41.4	15.1	1917	4	US-09-902-540-3588	Sequence 3588, Ap
43	41.4	15.1	19394	4	US-09-902-540-1172	Sequence 1172, Ap
44	41.4	15.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl
45	41.2	15.0	987	4	US-09-252-991A-13731	Sequence 13731, A

ALIGNMENTS

```

RESULT 1
US-09-583-110-44
; Sequence 44, Application US/09583110
; Patent No. 669703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 44
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; US-09-583-110-44

Query Match
Best Local Similarity 66.3%; Pred. No. 0.0077;
Matches 67; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 171 GACGATTTGAGAAATCGCCCTTCAAGAGCGGTGAGTGTGAGTCCGATGTC 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 GAAATTCGAGAAATGACAGTATCAAGTGTGAGTGTGAGTGTGAGTGTG 120

QY 231 CTCGCTTAGGACCGGCTTCAAGCGGCAAGCATGCCGTGCA 271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 GTTGAGCTTGAAGACGCTGAGTGTGATTTTGTGCA 161

RESULT 2
US-08-440-856A-9
; Sequence 9, Application US/08440856A
; Patent No. 5750873
; GENERAL INFORMATION:
; APPLICANT: DELLAPORTA, STEPHEN L.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
; TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVE. N.W.
; CITY: WASHINGTON

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/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/440,856A
/ FILING DATE: 15-MAY-1995
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MILLMAN, ROBERT A.
/ REGISTRATION NUMBER: 36,217
/ REFERENCE/DOCKET NUMBER: 05463-20001.00
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1517
/ TELEFAX: (202) 887-0763
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1288 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-440-856A-9

Query Match      16.3%; Score 46.4; DB 1; Length 1288;
Best Local Similarity 48.3%; Pred. No. 0.01;
Matches 86; Conservative 13; Mismatches 79; Indels 0; Gaps 0;

QY 97 TCATGCCACCGAAGAAAGCGGCATGAGACGGCGCTCTCTCCACCCCTCTCTCCCTCCG 156
Db 666 TCTCCGCTCCGACCGCTCGSGSGCTCTGCGCGCTCGCGCCGACGCTCACCCTCT 725
QY 157 TCATCCTCAACCCAGAAAGCATTTGAAGAAATCGCCGCTTACAAGAGCGCTGAGTACG 216
Db 726 CCAAGACGCCATCGTSGGCTCACCAAGACGCCCTCGCAGCTSSGCGSCACGCG 785
QY 217 AGTCGGGATGTCCTCTGCGCTTACGACCGCTTCCACCGCCCAAGCATGCGCTGACCG 274
Db 786 TCCGCTCAACTGCTCTCTGCGCTTGGCGTGGCCACSCSATGTCTCATCAACGCTG 843

RESULT 3
US-09-410-551B-1/c
/ Sequence 1, Application US/09410551B
/ Patent No. 6503737
/ GENERAL INFORMATION:
/ APPLICANT: KOSAN BIOSCIENCES, Inc.
/ APPLICANT: REEVES, CHRISTOPHER
/ APPLICANT: CHU, DANIEL
/ APPLICANT: KHOSLA, CHAITAN
/ APPLICANT: SANTI, DANIEL
/ APPLICANT: WU, KAI
/ TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
/ FILE REFERENCE: 30062-20026.00
/ CURRENT APPLICATION NUMBER: US/09/410,551B
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: US 60/139,650
/ PRIOR FILING DATE: 1999-06-17
/ PRIOR APPLICATION NUMBER: US 60/123,810
/ PRIOR FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: US 60/102,748
/ PRIOR FILING DATE: 1998-10-02
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 77536
/ TYPE: DNA
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/ ORGANISM: Streptomyces hygroscopicus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52275)...(71465)
/ US-09-410-551B-1

Query Match      16.3%; Score 44.6; DB 4; Length 77536;
Best Local Similarity 53.1%; Pred. No. 0.085;
Matches 95; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 96 TTGATGCCACCGAAGAAAGCGGCATGAGACGGCGCTCTCTCCACCCCTCTCTCCCTCC 155
Db 46351 TACTTCGCGCGCGCGCGCGCGCGCGCGCTGCGCTGCTCAACCGGACGCGCGGAC 46292
QY 156 GTGATCCTCAACCCAGAAAGCATTTGAAGAAATCGCGGCTTACAAGCGCGTGAATAGTG 215
Db 46291 GCCGAAGTGGCCCACTTCTGTACGAGATCTCCGCGGACCGTGTGTACACGAAAC 46232
QY 216 GAGTCGGGATGTCCTGCGCTTACGACCGGCTTCCACCGCCCAAGCATGCGTGCAGCG 274
Db 46231 CACTTCGACCAAGTGCAGCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGG 46173

RESULT 4
US-09-940-316B-1/c
/ Sequence 1, Application US/09940316B
/ Patent No. 6759536
/ GENERAL INFORMATION:
/ APPLICANT: KOSAN BIOSCIENCES, Inc.
/ APPLICANT: REEVES, CHRISTOPHER
/ APPLICANT: CHU, DANIEL
/ APPLICANT: KHOSLA, CHAITAN
/ APPLICANT: SANTI, DANIEL
/ APPLICANT: WU, KAI
/ TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE FK-520 POLYKETIDE SYNTH
/ FILE REFERENCE: 30062-20026.11
/ CURRENT APPLICATION NUMBER: US/09/940,316B
/ PRIOR FILING DATE: 2001-08-27
/ PRIOR APPLICATION NUMBER: 09/410,551
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: US 60/139,650
/ PRIOR FILING DATE: 1999-06-17
/ PRIOR APPLICATION NUMBER: US 60/123,810
/ PRIOR FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: US 60/102,748
/ PRIOR FILING DATE: 1998-10-02
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 77536
/ TYPE: DNA
/ ORGANISM: Streptomyces hygroscopicus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52275)...(71465)
/ US-09-940-316B-1

Query Match      16.3%; Score 44.6; DB 4; Length 77536;
Best Local Similarity 53.1%; Pred. No. 0.085;
Matches 95; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 96 TTGATGCCACCGAAGAAAGCGGCATGAGACGGCGCTCTCTCCACCCCTCTCTCCCTCC 155
Db 46351 TACTTCGCGCGCGCGCGCGCGCGCGCGCTGCGCTGCTCAACCGGACGCGCGGAC 46292
QY 156 GTGATCCTCAACCCAGAAAGCATTTGAAGAAATCGCGGCTTACAAGCGCGTGAATAGTG 215
Db 46291 GCCGAAGTGGCCCACTTCTGTACGAGATCTCCGCGGACCGTGTGTACACGAAAC 46232
QY 216 GAGTCGGGATGTCCTGCGCTTACGACCGGCTTCCACCGCCCAAGCATGCGTGCAGCG 274
Db 46231 CACTTCGACCAAGTGCAGCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGG 46173
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RESULT 5
US-09-103-840A-2
: Sequence 2, Application US/09103840A
: Patent No. 6294328
: GENERAL INFORMATION:
: APPLICANT: FLEISCHMAN, Robert D.
: APPLICANT: WHITE, Owen R.
: APPLICANT: FRASER, Claire M.
: APPLICANT: VENTER, John C.
: TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
: FILE REFERENCE: 24366-20007.00
: CURRENT APPLICATION NUMBER: US/09/103,840A
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 4403765
: TYPE: DNA
: ORGANISM: Mycobacterium tuberculosis
: FEATURE:
: OTHER INFORMATION: CDC 1551
: OTHER INFORMATION: "n" bases at various positions throughout the sequence
: OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          16.3%; Score 44.6; DB 3; Length 4403765;
Best Local Similarity 51.8%; Pred. No. 0.24;
Matches 101; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY      78  GCCATTCCCTAACCCCACTTTCATGCGCCACGAGAAACCGCGCATGAGACGCCGCTCTC 137
DB      1632416  GCCGCGCCCAACCGGCTCCCGCGGTGCGCCCGCAAGTCTCCGCGCGCGCGCGCGCC 1632475
QY      138  CACCCCTCTCTCCCTCCCTCGTCATCTCAACCAAGCATTTGAAGAAATGCGCGCTTAC 197
DB      1632476  CGCCCCCGCAAGCCCCCGCTTCTTGCGCTGTGCGGATTCGCGCGCGCGGTGGGCGA 1632535
QY      198  AAGGCGGTGAGTACGTGAGTCCGGGATGCTCGGCTTAGGACACCGGCTCCACCGCC 257
DB      1632536  GGAACCGGCGACACCGGCGCATGCGGTCCCGCCTTTGGCGCGCGCGCGCATTAACAAC 1632595
QY      258  AAGCATGCCGTGCGAC 272
DB      1632596  AAGCGCGCGGTGCC 1632610

RESULT 6
US-09-103-840A-1
: Sequence 1, Application US/09103840A
: Patent No. 6294328
: GENERAL INFORMATION:
: APPLICANT: FLEISCHMAN, Robert D.
: APPLICANT: WHITE, Owen R.
: APPLICANT: FRASER, Claire M.
: APPLICANT: VENTER, John C.
: TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
: FILE REFERENCE: 24366-20007.00
: CURRENT APPLICATION NUMBER: US/09/103,840A
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 4411529
: TYPE: DNA
: ORGANISM: Mycobacterium tuberculosis
: OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          16.3%; Score 44.6; DB 3; Length 4411529;

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Best Local Similarity 51.8%; Pred. No. 0.24; Indels 0; Gaps 0;
Matches 101; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY      78  GCCATTCCCTAACCCCATTTTCATGCGCACCGAAGAAACGGCCATGAGACGCCGCTTCTC 137
           |||
Db       1632529  GCCGGCCCCCAACCGGATCCCGCGTGCGCCCCCGAAGTCTCCCGCGCGCGCGCGCC 1632588
           |||

QY      138  CACCCTTCCTCCCTCCGTGCATCTCTCACCCAGACGATTTGAAGAAAATCGCGGCTTAC 197
           |||
Db       1632589  CGCCCGCCAGCCCCCGCGCTTCTGCGCGCTCTGTCGCGGATTCGCCCGCGCGGATGTGGGCGA 1632648
           |||

QY      198  AAGCGCTCGACGTAGTAGAGTCCGGCATGTCCTCGCGCTTAAGACAACGGCTCCACCGCC 257
           |||
Db       1632649  GGAACCGGCAACACCGGCGCATGCGCTTCCCGCGCTTTGCCCGGCGCGCGCATTAACAAC 1632708
           |||

QY      258  AACGATCCGCTGAC 272 -
           |||
Db       1632709  AAGCCCGCGCTTGCC 1632723
           |||

RESULT 7
US-09-133-321-1
; Sequence 1, Application US/09133321
; Patent No. 625558
GENERAL INFORMATION:
APPLICANT: Haeseloff, Phillip J.
APPLICANT: Hodge, Sarah
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 625558th Glebe Road, 8th Floor
CITY: Arlington
STATE: VA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/133,321
FILING DATE: 12-AUG-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9603069.7
FILING DATE: 14-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-452
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 17...694
US-09-133-321-1

Query Match          15.7%; Score 43; DB 3; Length 701;
Best Local Similarity 59.3%; Pred. No. 0.065;
Matches 73; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

120 ATGAGCGCGGCTCTCTCACCCCTCTCCCGCTCGGTACTCTCACCAAGACGATTTG 179
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Db 263 ATGACCTCTCCAGACATATAAAGCCCTGCTACCGGCTCTTCTGTCAGAGCAACGTG 322
QY 180 AAGAAATGCGCGCTCAACAGCGGCTCGAGTACGATGAGTCCGCGATGCTCGGGCTA 239
Db 323 AACAAAGCGCGCTCACCGACCGGCTGCTCGGTGAGACCGACATGCTCCCTACCTG 382
QY 240 GGC 242
Db 383 CGC 385

RESULT 8

US-09-252-991A-13584/C
Sequence 13584, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13584
LENGTH: 753
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13584

Query Match
Best Local Similarity 51.7%; Score 43; DB 4; Length 753;
Matches 100; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 80 CATTCCTACCCCATTTTCATGCGACGAGAAAGCGCGCATGACGGGCTCTCTCA 139
Db 283 CATGACCATTTCCAGCTCAGACGACCGTGGCGGCGGCAAGACTTACGGCTACCGCTG 224
QY 140 CCCCTCTCCCTCCCTCGTATCTCACCAGCAAGATTTGAAAGAAATGCGCGCTACAA 199
Db 223 CACCTCTCGGATGAGGCTGCGCCACCGCAGCATACCACTGAAAGGGGTCTCT 164
QY 200 GCGCGTCACTAGTACGTGAGTCCGCGATGCTCTCGGCTGAGGACCGGCTCAACCGCAA 259
Db 163 GAGCGCGCGGATCTGCAACGCGCGGAGATCGCCCTCTGCGCAACATTGCGCGGAT 104
QY 260 GCATGCGCTGACCG 274
Db 103 CGTCCCGCAGGCGCG 89

RESULT 9

US-09-252-991A-13860
Sequence 13860, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13860
LENGTH: 765

TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13860

Query Match
Best Local Similarity 51.3%; Score 43; DB 4; Length 765;
Matches 100; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 80 CATTCCTACCCCATTTTCATGCGACGAGAAAGCGGCTCTCTCTCA 139
Db 558 CATGACCATTTCCAGCTCAGACGACCGTGGCGGCGGCAAGACTTACGGCTACCGCTG 617
QY 140 CCCCTCTCCCTCCCTCGTATCTCACCAGCAAGATTTGAAAGAAATGCGCGCTACAA 199
Db 618 CACCTCTCGGATGAGGCTGCGCCACCGGCAATACCACTGAAAGGGGTCTCT 677
QY 200 GCGCGTCACTAGTACGTGAGTCCGCGATGCTCTGCGCTGAGGACCGGCTCAACCGCAA 259
Db 678 GAGCGCGCGGATCTGCAACGCGCGGAGATCGCCCTCTGCGCAACATTGCGCGGAT 737
QY 260 GCATGCGCTGACCG 274
Db 738 CGTCCCGCAGGCGCG 752

RESULT 10

US-09-103-840A-1/C
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match
Best Local Similarity 15.7%; Score 43; DB 3; Length 4411529;
Matches 100; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 78 GCGATTCCTTACCCCATTTTCATGCGACGAGAAAGCGGCTCTCTCTC 137
Db 927500 GCCGTACGAGCGCGAAGCGGCTCACCGGCGCGCTCCCGCGCTTCCCGCC 927441
QY 138 CACCCCTCTCCCTCCCTCGTATCTCACCAGCAAGATTTGAAAGAAATGCGCGCTTAC 197
Db 927440 GCGCGCGCGCGCGCGCTTACCGCGCTTGCAGATCAGCGCGGCTTGCAGCGCTCC 927381
QY 198 AAGCGCTGAGTACGTGAGTCCGCGATGCTCTGCGGCTAGGACCGGCTTCAACCGCC 257
Db 927380 GCGAGGCGCGCGAGGTGCTTGCAGGCGCGCGCGCGCGCGCGCGCGCGAGCC 927321
QY 258 AAGCAGCGCTGAC 272
Db 927320 GAACAGCAGGCGCG 927306

RESULT 11

US-09-902-540-8186
Sequence 8186, Application US/09902540
Patent No. 6833447

GENERAL INFORMATION:
 APPLICANT: Goldman, Barry S.
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Wiegand, Roger C.
 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 FILE REFERENCE: 38-10(15849)B
 CURRENT APPLICATION NUMBER: US/09/902,540
 PRIOR FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/217,883
 NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO 8186
 LENGTH: 2225
 TYPE: DNA
 ORGANISM: Myxococcus xanthus
 US-09-902-540-8186

Query Match 15.6%; Score 42.8; DB 4; Length 2225;
 Best Local Similarity 51.0%; Pred. No. 0.099; Indels 0; Gaps 0;
 Matches 101; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

76 TGGCATTCCCTACCCCATTTTCATCGCCAGAGAAAGCCGCATGAGCGCGCTCC 135
 905 TGGGCAAGACATTTCTCCGATCATTCCTCCAGAGAGACTTCCGCAAGCGCGCGCA 964
 136 TCCACCTCTCTCCCTCCCTCTGTCATCTTCAACCAAGACATTTGAAGAAATGCGCGCT 195
 965 TGCAGGAAGCCATCCGACCGCGCGCGCGCGCACAGAGAGCGCGCTCAAAACGCG 1024
 196 ACAAGCGCGTCAGTACGAGTCCGCGATGTCCTCGGCTAGGACCGCGCTCCACCG 255
 1025 ACGGAGCGTGTGACGCGAGGATCCACCATTTCTCTGCTTCGACGCGAGACT 1084
 256 CCAGCATGCCCTGACG 273
 1085 CCATGTTGCCGTCTCC 1102

RESULT 12
 US-09-902-540-842
 Sequence 842, Application US/09902540
 Patent No. 6833447
 GENERAL INFORMATION:
 APPLICANT: Goldman, Barry S.
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Wiegand, Roger C.
 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 FILE REFERENCE: 38-10(15849)B
 CURRENT APPLICATION NUMBER: US/09/902,540
 PRIOR FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/217,883
 NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO 842
 LENGTH: 6301
 TYPE: DNA
 ORGANISM: Myxococcus xanthus
 US-09-902-540-842

Query Match 15.6%; Score 42.8; DB 4; Length 6301;
 Best Local Similarity 51.0%; Pred. No. 0.13; Indels 0; Gaps 0;
 Matches 101; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
 76 TGGCATTCCCTACCCCATTTTCATCGCCAGAGAAAGCCGCATGAGCGCGCTCC 135
 4981 TGGGCAAGACATTTCTCCGATCATTCCTCCAGAGAGACTTCCGCAAGCGCGCGCA 5040
 136 TCCACCTCTCTCCCTCCCTCTGTCATCTTCAACCAAGACATTTGAAGAAATGCGCGCT 195
 5041 TGCAGGAAGCCATCCGACCGCGCGCGCGCGCACAGAGAGCGCGCTCAAAACGCG 5100

196 ACAAGCGCGTCAGTACGAGTCCGCGATGTCCTCGGCTAGGACCGGCTCCACCG 255
 5101 ACGGAGCGTGTGACGCGAGGATCCACCATTTCTCTGCTTCGACGCGAGACT 5160
 256 CCAGCATGCCCTGACG 273
 5161 CCATGTTGCCGTCTCC 5178

RESULT 13
 US-08-440-856A-2
 Sequence 2, Application US/08440856A
 Patent No. 5750873
 GENERAL INFORMATION:
 APPLICANT: DELAPORTA, STEPHEN L.
 TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
 TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 PENNSYLVANIA AVE. N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 15-MAY-1995
 APPLICATION NUMBER: US/08/440,856A
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: MILLMAN, ROBERT A.
 REGISTRATION NUMBER: 36,217
 TELEPHONE: (202) 887-1517
 TELEFAX: (202) 887-0763
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1187 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-440-856A-2

Query Match 15.4%; Score 42.2; DB 1; Length 1187;
 Best Local Similarity 50.2%; Pred. No. 0.12; Indels 0; Gaps 0;
 Matches 104; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
 68 CATTAACATGCGCATTCCTTACCCCATTTTCATGCGCACCGAGAAAGCCCATGAGCC 127
 551 CATGACCCAGCGCCGCGCGGAGCATCATCTCCGTCCGCAAGCGTCCGCGGTCTCTCC 610
 128 CGGCTCTCCACCGCCCTCTCCCTCCGTCATCTCAAGCAAGCAAGCAAGCAAGCAAG 187
 611 CGGCTCTCCACCGCCCTCTCCCTCCGTCATCTCAAGCAAGCAAGCAAGCAAGCAAG 670
 188 CGGCTCTCAAGCGCGTCTGAGTACGATGCGGATGCTCTCGGCTTGAAGCAAGCG 247
 671 CGGCTCTGAGTCTCGGCGCCACGAGCATCGCGGTCAATGCAATCTCCCTCTCGGCGT 730
 248 CTCACCGCGCAAGCATGCGGTGACCG 274
 731 CGGCAAGCGCATCATCAAGCGCTG 757

RESULT 14
 US-09-252-991A-6615/c

/ Sequence 6615, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 6615
/ LENGTH: 813
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6615

Query Match 15.3%; Score 42; DB 4; Length 813;
Best Local Similarity 48.0%; Pred. No. 0.12;
Matches 120; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 18 ACCACACATTCAATTGAACTCTGGAGCTGCTGACCTTCAACCTTTAATTACATG 77
DB 545 ACCGCGACAACTGACGACGAGTCTGCACTGTGTGTGAAGCTTCGAACCTTTGATG 486
QY 78 GCCATTCCCTACCCCATTTTCATTCGCCACCGAAGCCGCATGACGCGGCTCTTC 137
DB 485 GCCAATCCGACGACGAGTCCAAACCGACCAACAGCGCTCCGCGGATCAACGAATC 426
QY 138 CACCCCTCTCCCTCCCTCCGTCATCTCACCCAGACGATTTGAAGAAATCGCCCTAC 197
DB 425 GGGCGCGCGCCGACGAAATCGCCGGAACGCCCGCATGCCCTCGACATGCTTCGAC 366
QY 198 AAGCGCTGAGTAGTGAAGTCCGACATGCTCTCGGCTTAGGACCGGCTTCCACCGCC 257
DB 365 GCCAACACACAGCCGAGGACGCAACAGTGTGACAGACCATTCGCGCGATGAAC 306
QY 258 AAGCATGCCG 267
DB 305 GAGCTTTCCG 296

RESULT 15
US-09-252-991A-6683
/ Sequence 6683, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 6683
/ LENGTH: 1029
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6683

Query Match 15.3%; Score 42; DB 4; Length 1029;
Best Local Similarity 48.0%; Pred. No. 0.13;
Matches 120; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 18 ACCACACATTCAATTGAACTCTGGAGCTGCTGACCTTCAACCTTTAATTACATG 77

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Job time : 97.177 secs

DB 74 ACCGCGACAACTGACGACGATCTGCAACTGTGTGAACGCTCGAATCTTTCATG 133
QY 78 GCCATTCCCTACCCCATTTTCATTCGCCACCGAAGCCGCATGACCCGCGCTCTTC 137
DB 134 GCCAATCCGACGACGAGTCCAAACCGACCAACAGGTCGCGCGCATCAACGAATC 193
QY 138 CACCCCTCTCCCTCCCTCCGTCATCTCACCCAGACGATTTGAAGAAATCGCCCTAC 197
DB 194 GGGCGCGCGCCGACGAAATCGCCGCAACGCGCGATGCTTCGACCATGCTTCGAC 253
QY 198 AAGCGCTGAGTAGTGAAGTCCGACATGCTCTCGGCTTAGGACCGGCTTCCACCGCC 257
DB 254 GCCAACACACAGCCGAGGACGCAACAGTGTGACAGACCATTCGCGCGATGAAC 313
QY 258 AAGCATGCCG 267
DB 314 GAGCTTTCCG 323

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 310.867 Seconds
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Title: US-09-300-482-311

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Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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18: /cgn2_6/ptodata/1/pubna/US10F_PUBCOMB.seq:*
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22: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	274	100.0	274	US-09-987-899-4776	Sequence 4776, Ap
2	264.4	96.5	1422	US-10-425-114-15993	Sequence 15993, A
3	249	90.9	263	US-09-987-899-4775	Sequence 4775, Ap
4	230	83.9	1839	US-10-424-599-32036	Sequence 32036, A
5	189.6	69.2	1281	US-10-739-930-3349	Sequence 3349, Ap
6	189.6	69.2	1495	US-10-424-599-32035	Sequence 32035, A
7	160.2	58.5	244	US-10-424-599-90924	Sequence 90924, A
8	98	34.2	291	US-09-987-899-4779	Sequence 4779, Ap
9	93.8	34.2	265	US-09-987-899-4780	Sequence 4780, Ap
10	86.2	31.5	1027	US-10-739-930-3800	Sequence 3800, Ap
11	86	31.4	260	US-09-987-899-4781	Sequence 4781, Ap

12	86	31.4	705	18	US-10-425-115-133620	Sequence 133620,
13	86	31.4	1146	17	US-10-424-599-132085	Sequence 132085,
14	81.4	29.7	798	9	US-09-938-842A-656	Sequence 656, App
15	81.4	29.7	798	11	US-09-938-842A-656	Sequence 656, App
16	74.4	27.2	251	17	US-10-424-599-135774	Sequence 135774, A
17	69.4	25.3	1116	18	US-10-767-701-12123	Sequence 12123, A
18	64.8	23.6	1304	18	US-10-437-963-85192	Sequence 85192, A
19	63.6	23.2	436	17	US-10-424-599-36084	Sequence 36084, A
20	62.6	22.8	1585	18	US-10-425-115-138187	Sequence 138187, A
21	62.6	22.8	1606	18	US-10-739-930-2972	Sequence 2972, Ap
22	62.4	22.8	333	11	US-09-987-899-4766	Sequence 4766, Ap
23	62.4	22.8	1068	18	US-10-425-115-39573	Sequence 39573, A
24	61	22.3	1363	18	US-10-425-115-138189	Sequence 138189, A
25	59.4	21.7	267	11	US-09-987-899-4765	Sequence 4765, Ap
26	59.4	21.7	1004	18	US-10-739-930-2974	Sequence 2974, Ap
27	59.4	21.7	1480	18	US-10-739-930-2973	Sequence 2973, Ap
28	55.2	20.1	227	18	US-10-767-701-152	Sequence 152, App
29	54.6	19.9	4025	18	US-10-437-963-97674	Sequence 97674, A
30	50.4	18.4	299	17	US-10-424-599-84599	Sequence 84599, A
31	50.2	18.3	1060	17	US-10-425-114-6710	Sequence 6710, Ap
32	50.2	18.3	1136	17	US-10-425-114-35167	Sequence 35167, A
33	50.2	18.3	1392	18	US-10-425-115-107438	Sequence 107438, A
34	49.6	18.1	454	9	US-09-734-569-113	Sequence 113, App
35	48.2	17.6	951	15	US-10-156-761-719	Sequence 719, Appl
36	48.2	17.6	9025608	15	US-10-156-761-1	Sequence 1, Appl
37	48	17.5	796	18	US-10-437-963-40252	Sequence 40252, A
38	46.6	17.0	1128	18	US-10-437-963-96984	Sequence 96984, A
39	46.4	16.9	1206	18	US-10-437-963-85516	Sequence 85516, A
40	46.2	16.9	985	18	US-10-363-345A-31407	Sequence 31407, A
41	46.2	16.9	985	18	US-10-363-345A-31408	Sequence 31408, A
42	46.2	16.9	985	19	US-10-363-483A-31407	Sequence 31407, A
43	46.2	16.9	985	19	US-10-363-483A-31408	Sequence 31408, A
44	45.8	16.7	1055	18	US-10-739-930-4926	Sequence 4926, Ap
45	45	16.4	2731748	18	US-10-297-465A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-987-899-4776
Sequence 4776, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jingdong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262,979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076,712
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4776
LENGTH: 274
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700745725H1
US-09-987-899-4776

Query Match 100.0%, Score 274, DB 11, Length 274;
Best local similarity 100.0%, Pred. No. 6e-75;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACATTCCTTCCTCCACACACATTCATTTGACCTGAGACTGAGCTTCA 60
DB 1 CTACATTCCTTCCTCCACACACATTCATTTGACCTGAGACTGAGCTTCA 60

QY 61 CCTTAACATTAAATGAGCCATTCTTACCCCACTTTCATGCGCACCGAAGAACCGCCA 120
/ APPLICANT: Liu, Jindong
Db 61 CCTTAACATTAAATGAGCCATTCTTACCCCACTTTCATGCGCACCGAAGAACCGCCA 120
/ APPLICANT: Miller, Phillip W.
/ APPLICANT: O Connell, Keith M.
QY 121 TGAACGCGCGGCTCTCTCAACCCCTCTCCCTCGCATCTCCACCAAGACGATTGGA 180
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
/ FILE REFERENCE: 16517.258
Db 121 TGAACGCGCGGCTCTCTCAACCCCTCTCCCTCGCATCTCCACCAAGACGATTGGA 180
/ CURRENT APPLICATION NUMBER: US/09/987,899
QY 181 AGAAATCGCGCGCTTAACAAGCGCGTGAAGTGTGAGTCCGGCATGCTCGGCTTAG 240
/ PRIOR FILING DATE: 2001-11-16
Db 181 AGAAATCGCGCGCTTAACAAGCGCGTGAAGTGTGAGTCCGGCATGCTCGGCTTAG 240
/ PRIOR APPLICATION NUMBER: US 09/262,979
/ PRIOR FILING DATE: 1998-03-04
QY 241 GCACCGGCTCCACCGCGCAAGCATGCGGTGACCG 274
/ PRIOR FILING DATE: 1998-03-06
/ NUMBER OF SEQ ID NOS: 7341
Db 241 GCACCGGCTCCACCGCGCAAGCATGCGGTGACCG 274
/ SEQ ID NO 4775
/ LENGTH: 263
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 701120985H1

RESULT 2
US-10-425-114-19993

/ Sequence 19993, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53313) B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 19993
/ LENGTH: 1422
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB167-015-A9_FLI
US-10-425-114-19993

Query Match 96.5%; Score 264.4; DB 17; Length 1422;
Best Local Similarity 97.8%; Pred. No. 8.8e-72;
Matches 268; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTTAATTCCTTCTCCACGACATTTGAACCTTGGAGCTGAGCTTCAA 60
Db 222 CTTAATTCCTTCTCCACGACATTTGAACCTTGGAGCTGAGCTTCAA 281
QY 61 CCTTAACATTAAATGAGCCATTCTTACCCCACTTTCATGCGCACCGAAGAACCGCCA 120
Db 282 CCTTAACATTAAATGAGCCATTCTTACCCCACTTTCATGCGCACCGAAGAACCGCCA 341
QY 121 TGAACGCGGCTCTCTCAACCCCTCTCCCTCGCATCTCCACCAAGACGATTGGA 180
Db 342 TGAACGCGGCTCTCTCAACCCCTCTCCCTCGCATCTCCACCAAGACGATTGGA 401
QY 181 AGAAATCGCGCGCTTAACAAGCGCGTGAAGTGTGAGTCCGGCATGCTCGGCTTAG 240
Db 402 AGAAATCGCGCGCTTAACAAGCGCGTGAAGTGTGAGTCCGGCATGCTCGGCTTAG 461
QY 241 GCACCGGCTCCACCGCGCAAGCATGCGGTGACCG 274
Db 462 GCACCGGCTCCACCGCGCAAGCATGCGGTGACCG 495

RESULT 3
US-09-987-899-4775
/ Sequence 4775, Application US/09987899
/ Publication No. US20040116682A1
/ GENERAL INFORMATION:

/ APPLICANT: Cheikh, Nordine
/ APPLICANT: Liu, Jindong
/ APPLICANT: Miller, Phillip W.
/ APPLICANT: O Connell, Keith M.
QY 181 AGAAATCGCGCGCTTAACAAGCGCGTGAAGTGTGAGTCCGGCATGCTCGGCTTAG 240
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
/ FILE REFERENCE: 16517.258
Db 181 AGAAATCGCGCGCTTAACAAGCGCGTGAAGTGTGAGTCCGGCATGCTCGGCTTAG 240
/ CURRENT APPLICATION NUMBER: US/09/987,899
QY 241 GCACCGGCTCCACCGCGCAAGCATGCGGTGACCG 274
/ PRIOR FILING DATE: 2001-11-16
Db 241 GCACCGGCTCCACCGCGCAAGCATGCGGTGACCG 274
/ PRIOR APPLICATION NUMBER: US 09/262,979
/ PRIOR FILING DATE: 1998-03-04
QY 7341 GCACCGGCTCCACCGCGCAAGCATGCGGTGACCG 274
/ PRIOR FILING DATE: 1998-03-06
/ NUMBER OF SEQ ID NOS: 7341
/ SEQ ID NO 4775
/ LENGTH: 263
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 701120985H1

Query Match 90.9%; Score 249; DB 11; Length 263;
Best Local Similarity 98.1%; Pred. No. 3.4e-67;
Matches 252; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 181 AGAAATCGCGCGCTTAACAAGCGCGTGAAGTGTGAGTCCGGCATGCTCGGCTTAG 240
Db 1 ACCACACATTCAATTTGAACCTTGGAGCTGAGCTTCAAACCTTAACATTAAATG 60
QY 78 GCGATTCCTTCCCTCCCTCGCATCTCCACCAAGCATTTGAAGAAATGCGGCTTAC 137
Db 61 GCGATTCCTTCCCTCCCTCGCATCTCCACCAAGCATTTGAAGAAATGCGGCTTAC 120
QY 138 CACCCCTCTCCCTCCCTCGCATCTCCACCAAGCATTTGAAGAAATGCGGCTTAC 197
Db 121 CACCCCTCTCCCTCCCTCGCATCTCCACCAAGCATTTGAAGAAATGCGGCTTAC 180
QY 198 AAGCGCGTGAAGTGTGAGTCCGGCATGCTCGGCTTACCGGCTTACCGGCTTAC 257
Db 181 AAGCGCGTGAAGTGTGAGTCCGGCATGCTCGGCTTACCGGCTTACCGGCTTAC 240
QY 258 AAGCGCGTGAAGTGTGAGTCCGGCATGCTCGGCTTACCGGCTTACCGGCTTAC 274
Db 241 AAGCGCGTGAAGTGTGAGTCCGGCATGCTCGGCTTACCGGCTTACCGGCTTAC 257

RESULT 4
US-10-424-599-32036

/ Sequence 32036, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J
/ APPLICANT: Kovalic, David K
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53223) B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 32036
/ LENGTH: 1839
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1) ..(1839)
/ OTHER INFORMATION: unsure at all n locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_128934C.1
US-10-424-599-32036

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Query Match 3349, Application US/10739930
Best Local Similarity 89.7%; Pred. No. 4, 5e-61;
Matches 269; Conservative 0; Mismatches 5; Indels 26; Gaps 1;

QY 1 CTTACATTCCTTCTCCACACACATTCATTTTGAACCTGTGGAGCTGACTTCAA 60
DB 225 CTTACATTCCTTCTCCACACACATTCATTTTAAACCTGTGGAGCTGACTTCAA 294
QY 61 CCTTAAC-----ATTACATGGCCATTCCCTACCCCA 94
DB 295 CCTTAAACATGATGAGGCGCTCGGCTAGGACCGATTAACATGGCCATTCCCTACCCCA 354
QY 95 TTTATCGCCACCGAGAAAGCGCCATGAGCGCGGCTCTCTCCACCCCTCTCCCTC 154
DB 355 TTTATCGCCACCGAGAAAGCGCCATGAGCGCGGCTCTCTCCACCCCTCTCCCTC 414
QY 155 CGTCATCTCAACCCAGACGATTTTGAAGAAATGCGCGCTTCAAGAGCGGTGAGTACG 214
DB 415 CGTCATCTCAACCCAGACGATTTTGAAGAAATGCGCGCTTCAAGAGCGGTGAGTACG 474
QY 215 GGAGTCGGGCAATGCTCTCGGCTGAGGACCGGCTTCAACCGCAACATGCGGTGACCG 274
DB 475 GGAGTCGGGCAATGCTCTCGGCTGAGGACCGGCTTCAACCGCAACATGCGGTGACCG 534

RESULT 5
US-10-739-930-3349
; Sequence 3349, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 3349
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER2194_2
US-10-739-930-3349

Query Match 69, 2%; Score 189.6; DB 18; Length 1281;
Best Local Similarity 94.5%; Pred. No. 1, 4e-48;
Matches 208; Conservative 0; Mismatches 9; Indels 3; Gaps 1;

QY 58 CAACCTTAAACATTAACATGAGCCATTCCTTACCCCATTTTCAATGCGACGAGAAAGCG 117
DB 90 CACCATTAACTTAAACATGAGCCATTCCTTACCCCATTTTCAATGCGACGAGAAAGCG 149
QY 118 CCATGAGCGCGGCTCTCTCAACCCCTCTCTCC--CTTCGATCTTACCCCAAGAG 174
DB 150 CCATGAGCGCGGCTCTCTCAACCCCTCTCTCCCTCTCCGTCATCTTCAACCAAGAG 209
QY 175 ATTGGAAGAAATGCGCGCTTCAAGAGCGCGTGAAGTACGTGAGTCCGGCAGAGTCTCTG 234
DB 210 ACCTTAAGAAATGCGCGCTTCAAGAGCGCGTGAAGTACGTGAGTCCGGCAGAGTCTCTG 269
QY 235 GCCTAGGACCGGCTTCAACCGCAAGCATGCGTGAAGCG 274
DB 270 GCCTAGGACCGGCTTCAACCGCAAGCATGCGTGAAGCG 309

RESULT 6
US-10-424-599-32035
; Sequence 32035, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

```

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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ. ID NOS: 285684
SEQ ID NO 32035
LENGTH: 1495
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_128933C.1
US-10-424-599-32035

Query Match
Best Local Similarity 69.2%; Score 189.6; DB 17; Length 1495;
Matches 209; Conservative 0; Mismatches 9; Indels 3; Gaps 1;

QY 58 CAACCTTTAACTTAACATGCGCATTCCTCAATCCCACTTTGATGCGCAGCAAGAGCCG 117
DB 305 CACCCCTTAACATTAACATGCGCATTCCTCAATCCCACTTTGATGCGCAGCAAGAGCCG 364

QY 118 CCATGAGACGGCGGCTCTCCACCCCTCTCCCTCCGCGATCTTACCCCAAGAGC 174
DB 365 CCATGAGACGGCGGCTCTCCACCCCTCTCCCTCCGCGATCTTACCCCAAGAGC 424

QY 175 ATTGAAGAAATTCGCGCGCTTACAGAGCGCTGAGTACGTGAGTCCGCGATGCTCTCG 234
DB 425 ACCTCAGAAATTCGCGCGCTTACAGAGCGCTGAGTACGTGAGTCCGCGATGCTCTCG 484

QY 235 GCCTAGGACCGGCTCCACCGCCCAAGCATGCGCTGACCG 274
DB 485 GCCTAGGACCGGCTCCACCGCCCAAGCATGCGCTGACCG 524

RESULT 7
US-10-424-599-90924
Sequence 90924, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ. ID NOS: 285684
SEQ ID NO 90924
LENGTH: 244
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)-(244)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_53115C.1
US-10-424-599-90924

Query Match
Best Local Similarity 58.5%; Score 160.2; DB 17; Length 244;
Matches 197; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 17 CACCACACATTCATTTTGAACCTCTGGACCTGCTAGCTTCAACCTTTAACTTAACAT 76
DB 3 CACCACACATTCATTTTGAACCAACTCGGGGAGGCTCTTAACTTAACATTAACAT 62

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;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
;; FILE REFERENCE: 16517.258
;; CURRENT APPLICATION NUMBER: US/09/987,899
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: US 09/262,979
;; PRIOR FILING DATE: 1999-03-04
;; PRIOR APPLICATION NUMBER: US 60/076,712
;; PRIOR FILING DATE: 1998-03-06
;; NUMBER OF SEQ ID NOS: 7341
;; SEQ ID NO 4781
;; LENGTH: 260
;; TYPE: DNA
;; ORGANISM: Glycine max
;; FEATURE:
;; OTHER INFORMATION: Clone ID: 701120413H1
US-09-987-899-4781

Query Match
Best Local Similarity 31.4%; Score 86; DB 11; Length 260;
Matches 107; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 131 CCTCTCCACCCCTCTCCCTCCCTCCCTCATCTCACCACCAAGAGATTGAAGAAATCGC 190
DB 68 CCACTCCCTCCCTCCCTCCCTCCCTCCCTCATCTCACCACCAAGAGATTGAAGAAATCGC 127

QY 191 CCGCTTACAAGGCGGTGAGTAGTGGAGTCCGGCATGTCTCTCGGCTTACGACCGGCTC 250
DB 128 CCGCTTACAAGGCGGTGAGTAGTGGAGTCCGGCATGTCTCTCGGCTTACGACCGGCTC 187

QY 251 CACCGCAAGCATGCCGTGAC 272
DB 188 CACTGCTGCTTCTGTGTGCGC 209

RESULT 12
US-10-425-115-133620
;; Sequence 133620, Application US/10425115
;; Publication No. US20040214272A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;; FILE REFERENCE: 38-21(53222)B
;; CURRENT APPLICATION NUMBER: US/10/425,115
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 369326
;; SEQ ID NO 133620
;; LENGTH: 705
;; TYPE: DNA
;; ORGANISM: Zea mays
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (1)..(705)
;; OTHER INFORMATION: unsure at all n locations
;; FEATURE:
;; OTHER INFORMATION: Clone ID: MRT4577_53350C.1
US-10-425-115-133620

Query Match
Best Local Similarity 31.4%; Score 86; DB 18; Length 705;
Matches 107; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 131 CCGCTTACAAGGCGGTGAGTAGTGGAGTCCGGCATGTCTCTCGGCTTACGACCGGCTC 190
DB 176 CCACTCCCTCCCTCCCTCCCTCCCTCCCTCATCTCACCACCAAGAGATTGAAGAAATCGC 235

QY 191 CCGCTTACAAGGCGGTGAGTAGTGGAGTCCGGCATGTCTCTCGGCTTACGACCGGCTC 250
DB 236 CCGCTTACAAGGCGGTGAGTAGTGGAGTCCGGCATGTCTCTCGGCTTACGACCGGCTC 295

QY 251 CACCGCAAGCATGCCGTGAC 272
DB 296 CACTGCTGCTTCTGTGTGCGC 317

RESULT 13
US-10-424-599-132085
;; Sequence 132085, Application US/10424599
;; Publication No. US20040031072A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;; FILE REFERENCE: 38-21(53223)B
;; CURRENT APPLICATION NUMBER: US/10/424,599
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 285684
;; SEQ ID NO 132085
;; LENGTH: 1146
;; TYPE: DNA
;; ORGANISM: Glycine max
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (1)..(1146)
;; OTHER INFORMATION: unsure at all n locations
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT3847_90280C.1
US-10-424-599-132085

Query Match
Best Local Similarity 31.4%; Score 86; DB 17; Length 1146;
Matches 107; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 131 CCTCTCCACCCCTCTCTCCCTCCCTCCCTCATCTCACCACCAAGAGATTGAAGAAATCGC 190
DB 247 CCACTCCCTCCCTCCCTCCCTCCCTCCCTCATCTCACCACCAAGAGATTGAAGAAATCGC 306

QY 191 CCGCTTACAAGGCGGTGAGTAGTGGAGTCCGGCATGTCTCTCGGCTTACGACCGGCTC 250
DB 307 CCGCTTACAAGGCGGTGAGTAGTGGAGTCCGGCATGTCTCTCGGCTTACGACCGGCTC 366

QY 251 CACCGCAAGCATGCCGTGAC 272
DB 367 CACTGCTGCTTCTGTGTGCGC 388

RESULT 14
US-09-938-842A-656
;; Sequence 656, Application US/09938842A
;; Patent No. US20020160378A1
;; GENERAL INFORMATION:
;; APPLICANT: Harper, Jeff
;; APPLICANT: Krieps, Joel
;; APPLICANT: Wang, Xun
;; APPLICANT: Zhu, Tong
;; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;; FILE REFERENCE: SRIPI300-3
;; CURRENT APPLICATION NUMBER: US/09/938,842A
;; CURRENT FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: US 60/227,866
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: US 60/264,647
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/300,111
;; PRIOR FILING DATE: 2001-06-22
;; NUMBER OF SEQ ID NOS: 5379
;; SEQ ID NO 656
;; LENGTH: 798

TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-656

Search completed: May 4, 2005, 21:11:46
Job time : 316.867 secs

Query Match 29.7% Score 81.4; DB 9; Length 798;
Best Local Similarity 64.7%; Pred. No. 5,1e-15;
Matches 121; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 88 ACCCCCATTTTCATCGCCACCGAAGACCGCCATGAGCCGCGCTTCCTCCACCCCTCCT 147
DB 17 ATCTCTCTTCAATTAACACAGACGCTCAAGCTATGCGCGCTTACAAAGCCGTGG 76
QY 148 CCCCCCTCCATCCATCCACCAAGACGATTTGAAGAAATGCGCGCTTACAGCGCTCG 207
DB 77 CTCAGCCCATGATTAATTAACACAGACGCTCAAGCTATGCGCGCTTACAAAGCCGTGG 136
QY 208 AGTAGGTGAGTCCGCGATGCTCTCGGCTTAGGCAACCGGCTCCACCGCCAAAGCATGCGG 267
DB 137 AATTGTCGAGTCGGGATGTTCTCGGCTTCGGAACCGGCTCCACCGCCAAAGCATGCGG 196
QY 268 TCGACCG 274
DB 197 TCGACCG 203

RESULT 15

US-09-938-842A-656
Sequence 656, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 656
LENGTH: 798
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-656

Query Match 29.7% Score 81.4; DB 11; Length 798;
Best Local Similarity 64.7%; Pred. No. 5,1e-15;
Matches 121; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 88 ACCCCCATTTTCATCGCCACCGAAGACCGCCATGAGCCGCGCTTCCTCCACCCCTCCT 147
DB 17 ATCTCTCTTCAATTAACACAGACGCTCAAGCTATGCGCGCTTACAAAGCCGTGG 76
QY 148 CCCCCCTCCATCCATCCACCAAGACGATTTGAAGAAATGCGCGCTTACAGCGCTCG 207
DB 77 CTCAGCCCATGATTAATTAACACAGACGCTCAAGCTATGCGCGCTTACAAAGCCGTGG 136
QY 208 AGTAGGTGAGTCCGCGATGCTCTCGGCTTAGGCAACCGGCTCCACCGCCAAAGCATGCGG 267
DB 137 AATTGTCGAGTCGGGATGTTCTCGGCTTCGGAACCGGCTCCACCGCCAAAGCATGCGG 196
QY 268 TCGACCG 274
DB 197 TCGACCG 203

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 112.658 Seconds
(without alignments)
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Title: US-09-300-482-356

Sequence: 1 caaccggcaccacgctgac.....acgctcggagctttttt 385

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	170.4	44.3	2629	2	US-09-012-030-1
2	170.4	44.3	2629	2	US-08-590-454-1
3	116.2	30.2	2007	4	US-09-252-991A-3308
4	116.2	30.2	2229	4	US-09-252-991A-3240
5	116.2	30.2	2709	4	US-09-382-106-1
6	114.6	28.8	1998	3	US-09-382-106-1
7	106.2	27.6	2085	4	US-09-489-039A-1895
8	100.4	26.1	2127	4	US-09-489-039A-4813
9	99	25.7	35881	4	US-08-311-731A-127
10	93.8	24.4	6895	4	US-09-531-266-1
11	85.8	22.3	4403765	3	US-09-103-840A-2
12	85.8	22.3	4411529	3	US-09-103-840A-1
13	82.8	21.5	2143	3	US-09-064-693A-18
14	82.8	21.5	6641	3	US-09-064-693A-25
15	80.6	20.9	11443	3	US-08-961-527-49
16	80	20.8	1953	4	US-08-956-171E-374
17	80	20.8	1953	4	US-08-956-171E-374
18	78.2	20.3	1968	3	US-09-298-724-1
19	78.2	20.3	1971	4	US-09-583-110-597
20	78.2	20.3	1980	4	US-09-107-433-1992
21	76.8	19.9	1995	5	PCT-US96-05330A-1025
22	76.8	19.9	1830121	4	US-09-557-884-1
23	76.8	19.9	1830121	4	US-09-643-990A-1
24	76.4	19.0	2028	3	US-09-134-001C-2382
25	73	17.7	1230230	4	US-09-438-185A-1
26	68	17.7	1230230	4	US-09-438-185A-1
27	65.8	17.1	1854	4	US-09-107-433-1993

ALIGNMENTS

28	65.8	17.1	1977	4	US-09-583-110-2082	Sequence 2082, Ap
29	64.2	16.7	837	4	US-09-134-000C-201	Sequence 201, Ap
30	63.6	16.5	1998	4	US-09-543-681A-1706	Sequence 1706, Ap
31	63	16.4	1738	3	US-08-858-207A-35	Sequence 35, Ap
32	56.8	14.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli
33	53.8	14.0	946	3	US-08-961-527-239	Sequence 239, Ap
34	51.6	13.5	1329	4	US-09-252-991A-3367	Sequence 3367, Ap
35	51.6	13.4	1359	4	US-09-252-991A-3294	Sequence 3294, Ap
36	51.6	13.4	1377	4	US-09-252-991A-3340	Sequence 3340, Ap
37	51.6	13.4	1710	4	US-09-252-991A-3383	Sequence 3383, Ap
38	51.6	13.4	1872	2	US-08-743-637B-17	Sequence 17, Appl
39	51.6	13.4	1872	3	US-08-526-840B-17	Sequence 17, Appl
40	48.2	12.5	615	4	US-09-540-236-214	Sequence 214, Ap
41	48.2	12.5	99629	4	US-09-596-002-37	Sequence 37, Appl
42	44	11.4	1284	3	US-09-327-487A-4	Sequence 4, Appli
43	43.4	11.3	1059	4	US-09-902-540-2579	Sequence 2579, Ap
44	43.4	11.3	14342	4	US-09-902-540-1118	Sequence 1118, Ap
45	43	11.2	1281	3	US-09-327-487A-3	Sequence 3, Appli

RESULT 1
US-09-012-030-1
Sequence 1, Application US/09012030
Patent No. 5912169
GENERAL INFORMATION:
APPLICANT: SCHMIDT, Ralf-Michael, STITTL, Marc, SONNEWALD,
APPLICANT: Uwe
TITLE OF INVENTION: Transketolase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Keil & Weinkeuf
STREET: 1101 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: Wordperfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012, 030
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,454
FILING DATE: 22-JAN-1996
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2629 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Nicotiana
FEATURE:
NAME/KEY: CDA
LOCATION: 60..2289
US-09-012-030-1
Query Match 44.3%; Score 170.4; DB 2; Length 2629;
Best Local Similarity 67.4%; Pred. No. 3e-39;
Matches 240; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
4 CCGGACCAAGGCTGACATCATTTGGGTGGGACCGGCTCGAGCTGAGATCGGGGCA 63
DB 1936 CTGGCAACAACTGATGATCTTTGATTTGGTACTGCTCAGATTAGAAATGCTGTCA 1995

QY 64 ATGCGGCGCAGCTGAGGAAGAGGGGAAGCGGTCCGCGCTGCTGCTCCT 123

Db 1996 AGGCTGCTGATGAATCTCAGGAAAGAGAAAGAAAGCACTGAGAGTGTGTTCTTGTGTT 205

QY 124 GGGAACTCTTTGATGAGCAGTCCGATGACTACAAAGAGAGCGTCTCTCCCTGCCAGCTGA 183

Db 2056 GGGACCTTTTGGAAAMAACATCAGCCGACTAACAGGAAGTGTCTTTCATCATCTGTTA 211

QY 184 CAGCAGAGATCAGATCGAGGCGCGGATCCACTCGGCTGGGAGAAAGTACGTCCGAGCCC 243

Db 2116 CAGCTAGAGTTAGCATTTGAGGCCGATCCACTTTGGTGGGAGAAATATGTGCGATCAA 217

QY 244 AAGGTAAGGCCATTGGCATCGACAAGTTGCGCGCGAGTCTCTGCGCGGACGATCTACA 303

Db 2176 AGGGGAAGCCCATCGGAATTGACAATGGGGGCCAGTGCCTCTCGGAAAAATATACA 223

QY 304 AGGAGTACGGGATCACCGTGGAGAGCATCATTCGAACTGCCAAGAGCTTTTAAAGG 359

Db 2236 AGGAGTACGGAATTACAGACAGAGGCGTGTGTGACTGCTCAGCTTAAACAAGTTTCTTAG 2291

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US-08-590-454-1
: Sequence 1, Application US/08590454
: Patent No. 592535
: GENERAL INFORMATION:
: APPLICANT: SCHMIDT, Ralf-Michael, STITZ, Marc, SONNEMALD,
: APPLICANT: Uwe
: TITLE OF INVENTION: Transketolase
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kell & Weinkauff
: STREET: 1101 Connecticut Avenue
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
: COMPUTER: IBM AT-compatible, 80486 processor
: OPERATING SYSTEM: MS-DOS version 6.0
: SOFTWARE: Wordperfect version 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/590.454
: FILING DATE: 22-JAN-1996
: CLASSIFICATION: 435
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2629 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ORIGINAL SOURCE:
: ORGANISM: Nicotiana
: FEATURE:
: NAME/KEY: CDA
: LOCATION: 60..2289
: US-08-590-454-1

Query Match      44.3%; Score 170.4; DB 2; Length 2629;
Best Local Similarity 67.4%; Pred. No. 3e-39;
Matches 240; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

4 CCGGACCAACCCGATCATCTTGGCTTGGGCACCGGCTCCGAGCTGGAGATCGCGGACA 63
dbp CTTGGCAACAACCTCGATGTCATTTTGTATTGTCCTGACTGAGTGAATTAATTCCTGCA 1995
1996 AGGCTGCTGATGAACCTAGGAAAGCAAGAAAGCAAGCAAGTGTGTTTCTTTGTTGTT 2055
64 ATGCGGCGCAGACGACTGAGAGAGGAGGAGAAACGGCTCGCGCTCGCTCGCTCTCT 123

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QY 124 GGGAACTTTTGAAGACAGTCGGATAGTACAAGAGAGAGGCTCTCCCTCCGACCTCA 183

Db 2056 GGGAGCTTTTGAAGAACATCAGCCGACTCAAGAAAGTGTCTTCATCATCTGTTA 2115

QY 184 CAGCGAGGATCAGCATCGAGCCCGGCTCACTCGGCTGGCAGAAAGTACGTGGAGGCC 243

Db 2116 CAGCTAGATTAGCATTTGAGGCGGATTCACATTTGGGTGGAGAAATATGTCCGATCA 2175

QY 244 AAGCCAAAGCCATTGGCATGACAAAGTTGGGCGCGAGTGCTCTGCGCGGAGCATTTACA 303

Db 2176 AGGGGAAGGCGATCGCAATTGACAGAGGGGATGCGCATGCCCCCTGCAAAAATATACA 2235

QY 304 AGGAGTACGGCATCACCGTGGAGAGCATCAATTGCAATGCGCAAGAGCTTTTAAGAG 359

Db 2236 AGGAGTACGGAAATTACGACAGAGCGCTGTGTAGCTGAGGCTTAACAAGATTTCTTAA 2291

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RESULT 3
US-09-252-991A-3308
/ Sequence 3308, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 3308
/ LENGTH: 2007
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3308

Query Match      30.2%; Score 116.2; DB 4; Length 2007;
Best Local Similarity 59.1%; Pred. No. 1.2e-23;
Matches 199; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY      11 CAACCTCGATCATCTTTGGTTGGGCACCGGCTCCGAGCTGGAGATCGGGCAATCGCG 70
DB      589 CGACCCCGAACTGATCTCTGATCGCACCCGGTTGCGAAGTGCAGCTGCGTGCAGCCCTTA 648
QY      71 CGACGAGCTGAGGAGGAGGAGGAGGAGACCGGTCGCGTCTGTTGCTCTCTTGGGAAT 130
DB      649 CGACAACTCAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 708
QY      131 CTTGATGAGCACTCGGATGAGTACAAGAGAGACGTCCTCCCTGCCAGATCAGACCGAG 190
DB      709 CTACGAGCACAAGAGAGAGAGTCTTACAAGCAGTCCGATGCTGCGGATGGAAGTCCGCGCG 768
QY      191 GATCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 250
DB      769 CATGCGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 828
QY      251 GGCATATGGCATGAGCAAGTTCGAGCGAGAGTGCTCTGCGGGAGAGATCTACAAGAGTA 310
DB      829 CATCATTCGAGATACCAAGCTTCGAGCGAGTTCGAGCGAGGAGGAGGAGGAGGAGGAGG 888
QY      311 CGGCAATCAGCGTGGAGAGATCATTTGCCAATCGCCAA 347
DB      889 CGGCTTACCCCTGAGCAAGTCTCTGCGGATGCGAG 925

```

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? GENERAL INFORMATION:
? APPLICANT: Marc J. Rubenfield et al.
? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
? TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
? FILE REFERENCE: 107196.136
? CURRENT APPLICATION NUMBER: US/09/252,991A
? CURRENT FILING DATE: 1999-02-18
? PRIOR APPLICATION NUMBER: US 60/074,788
? PRIOR FILING DATE: 1998-02-18
? PRIOR APPLICATION NUMBER: US 60/094,190
? PRIOR FILING DATE: 1998-07-27
? NUMBER OF SEQ ID NOS: 33142
? SEQ ID NO 3240
? LENGTH: 2229
? TYPE: DNA
? ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3240

```

Query Match	30.2%;	Score 116.2;	DB 4;	Length 2229;
Best Local Similarity	59.1%;	Pred. No. 1.3e-23;		
Matches 199; Conservative	0;	Mismatches 138;	Indels 0;	Gaps 0;

QY	11	CAACCTTGACATCAATTGGGTTGGGACCCGGCTCCAGCTCGAGATCGAGGCAATGCGGC	70
Db	1875	CGACCTCGGAATCGATCTCGATTCGACCACCGGTTCCGAATCGGCGCTGGCCGTGACAGCTTA	1934
QY	71	CGACGACGTGAGGAAGAGGAGGAGACGGTCCGCGTCTGCTTCCTGCTGCTCTCTGGAAACT	130
Db	1935	CGACAAAGCTCAGCAGACGACGGGCCCGCAAGTCCGCGCTGGATTCGATCGACATGCACCAAGCT	1994
QY	131	CTTTGATGAGCAGTCGATCGATGAGTACAAAGAGAGCGTCTCTCCCTCCGACGTCAACAGCAG	190
Db	1995	CTACGAGAGCAGGACGAGTCTCTAACACAGTCGCTGTGCTGCACGATGGAAGTCCGCGCCG	2054
QY	191	GATACGATCGAAGCCCGAGTCCACTCTTGCGCTGGCAGAAATGCTTCGAGGCCCAAGCGAA	250
Db	2055	CATGCGCATCGAGGCCCGCCCAATGCCGATCTACTGTGTACAAAGTACGTCGGTCTTCGACGGGCG	2114
QY	251	GGCCATTGGCATCGACAAGTTCCGCGCCAGTGTCTTCCCGGACGATCTACAAAGAGTA	310
Db	2115	CATCATCGGCGATGACAGCTTCCTGGGAGATCGGCGCCGCCCGGCGCTGTTGAGCACTT	2174
QY	311	CGGCATCAACCTGGAGAGACATCTTGCACATGCCAAG	347
Db	2175	CGGCTTACCCCTGGACAAACGTCCTGGCGCGTAGCCGAG	2211

```

RESULT 5
US-09-252-991A-3326/C
; Sequence 3326, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196, 136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3326
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-3326

```

Query Match	30.2%	Score 116.2;	DB 4;	Length 2709;
Best Local Similarity	59.1%;	Pred. No. 1.4e-23;		
Matches 199; Conservative	0;	Mismatches 138;	Indels 0;	Gaps 0;

QY 1 CAGCGTCGATCATTTGGGTTGGGACCGGCTCCGAGTGGAGATCCGCGGGCATGGGC 70
Db 976 CGAGCCGGAACTGATCTTGATGCGACCGGTTCCGAAAGTCGGCTGGCCGTGCAAGGCTTA 917
QY 71 CGACGAGCTGAGGAAGAGGGGAGACGGTCGGGTCGTCTGTTCTCTCTGGGAAT 130
Db 916 CGACGAGCTCAGCGAGACGGGCGCGAAGTCTCGGGTGGTATCGATGCGATGCACACAGCGT 857
QY 131 CTTTGATGAGCAGTCGGATGAGTACAGAGAGCGTCTCTCCCTGCGACGTCAACGCGAG 190
Db 856 CTTCGAGCAGCAGACGACGAGTCTTACAAACATCCGTCTCGCTCGGTGGAAATCGGCGCGCG 797
QY 191 GATCAGCATCCGAGGCGCGGCTCCACTCTCGGCTGGCAGAAAGTACTCGGACCCCAAGCAA 250
Db 796 CATCGGCATCCGAGGCGCGGCCCATGCGACTTGTGTATCAAGTACGTCCGTCTCGACGGGCG 737
QY 251 GGCATTGGCATCGACAAGTTGGGCGCGAGTCTCTGCGGGAGCAATCTTACAAGAGTA 310
Db 736 CATCATCGGCATGACCACTGTTGGGCGAATCGGCGCGCGGCCGCTGTTCCAGCACTT 677
QY 311 CGGCATCACCGTGAGAGAGCATCATTCACAAGTCCAAAG 347
Db 676 CGGCTTCACTCGACAAAGTCTCTGGCGGTAGCCGAG 640

```

? RESULT 6
? US-09-382-106-1
? Sequence 1, Application US/09382106
? Patent No. 6221631
? GENERAL INFORMATION:
? APPLICANT: Huang, Jianzhong
? APPLICANT: Jiang, Xinhe
? APPLICANT: McDevilt, Damien
? APPLICANT: Van Horn, Stephanie
? TITLE OF INVENTION: ctkA
? FILE REFERENCE: GM10236
? CURRENT APPLICATION NUMBER: US/09/382,106
? CURRENT FILING DATE: 1999-08-24
? NUMBER OF SEQ ID NOS: 2
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 1
? LENGTH: 1998
? TYPE: DNA
? ORGANISM: Pseudomonas aeruginosa
? US-09-382-106-1

```

Query Match	29.8%	Score 114.6	DB 3	Length 1998
Best Local Similarity	58.8%	Pred. No. 3,56-23		
Matches 198	Conservative	0	Mismatches 139	Indels 0
			Gaps	0
QY	11	CAAGCTTGACATCATTTGGGTTGGGCAACGGGCTCCGAGCTGGAGATCGCGGGCATATCGGC	70	
Db	1644	CGAGCCCGGAATCGATCTGATGCGACCGGTTGGGAAGTGGGCTGGCGCTGACAGGCGTAA	170	
QY	71	CGACGAGCTTGAGGAAGAGGGGGAAGACGGTCCGCTGCTCGTTCTCTCTGGGAATCT	130	
Db	1704	CGACAGAGCTCAACGAGCAGCGGCGCCGACAGGTCCGGTGGTATCGATGCCATGACACAGCGT	176	
QY	131	CTTTGATGAGCAGTGGGATGAGTCAAGAGAAAGGCTCTCCCTCGCAAGCTCACACGAG	190	
Db	1764	CTACGAGCAGCGGAGCGAGTCCCTTCACAGCAATCTCGTCTCCGGTGAATTCGGCCCGG	182	
QY	191	GATCAGCATCGAGGCGCGGAGTCCACTCTCGGTGGCCAGAAAGTATCGAGCCCAAGGCAA	250	
Db	1824	CATCGCATCGAGGCGCGCCCATGCCAGTACTGTCTAAATAGTCTCGTCTCCACGCGGG	188	
QY	251	GGCCATTTGGCATCGACAAATTTGGGCGCGAGTCTCTGCGCGGAGCATCTCAAGGAGTAA	310	
Db	1884	CATCATCGGCATGACACAGCTTCGGGAGATCGGCCCGGCCCGGCGCTGTCGAGACATT	194	
QY	311	CGGCATCACCGTGGAGAGAGCATTTGCAATCTGCCAAG	347	
Db	1944	CGGCTTCAACCTTGACCAAGTCTCTGGCGGTGGGGAG	1980	

```

RESULT 7
US-09-489-039A-1895
; Sequence 1895, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709, 2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1895
; LENGTH: 2085
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1895

```

	Query Match Best Local Similarity	27.6% 56.9%	Score 106.2	DB 4	Length 2085
	Matches 195	Conservative 0	Mismatches 148	Indels 0	Gaps 0
QY	4	CCGGCACCMAACCCTTACATCATTTGGGTTGGGGACCGGCTCCGAGCTGGAGATCGGGGCA	63		
Db	1724	CCGGCGGCAAGCCCGACCTGATCTCTCATGCGCACCCGGCTCGGAAGTGAATCACCCTCC	178		
QY	64	ATGCGGCGCGACGAGCTGAGAGAAAGAGGGGAGACGGTCCGCTGCTCTTGTCGTCCTCT	123		
Db	1784	TGGCCGCGGAAAAACTGTTGGCCAAAGGGGTAAATGTGCGGGTCTGTCCGCTCCCTTCCA	184		
QY	124	GGGAACCTCTTTGATATAGCAGCTCGATGTAAGTACAAAGAAAGGCTCTCCCTGCCACGTCA	183		
Db	1844	CTGATGTTTGTGAAGCCCAAGATGAGGCGCTGGCGGAATCGGTGTGCGTGGCACTCA	1903		
QY	184	CAGCGAGATCAGCATCGAGGCCGGGGTCCACTCTCGGCTGGCAGAAATACGTCGAGGCC	243		
Db	1804	GCGCCGGGGTGGCGGATCGAAGCCGGGAATAGGGAATCTGGTATTAATATGTGGCTTAA	1963		
QY	244	AAGCCAAAGGCATTGGCATTCGACAAATTGCGCGCGAGTGCTCTGCCCGGACGATTTACA	303		
Db	1964	AAGGCAAGATGTGGCGCATGACCGGCTATGGCGAATCGGCCCGGCAAGCAAGTTGTTCC	2023		
QY	304	AGGAGTACGGCATCACCGTGGAGAGCATTCATTGCAATCGCCAA	346		
Db	2024	CGTCTTTGGCTTTAAGGTGCAATATCGTCCGACCGCCGA	2066		

RESULT 8
 US-09-489-039A-4813
 ; Sequence 4813, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709 2004001
 ; CURRENT APPLICATION NUMBER: US/09/489, 039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 4813
 ; LENGTH: 2127
 ; TYPE: DNA
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-4813

Query Match	26.1%;	Score 100.4;	DB 4;	Length 2127,
Best Local Similarity	55.8%;	Pred. No. 4.6e-19;		

	Matches	191;	Conservative	0;	Mismatches	151;	Indels	0;	Gaps	0;
QY	5	CGGCACCAAGCCTGACATCATTTGGGTTGGGACCCGGCTCCGAGCTGGAGATCGCGGGCAA	64							
Db	1773	CGCCGGCCGACCGGAGCGTGTGATCTTCATCGCCACCGGTTCAAGAATGGAGTGGGGGTTGC	1833							
QY	65	TGCGGCGCAGAGGTGAGGAGAGAGGGGANAACGCTCCGCTCGTTCGTTCGTTCTCTG	124							
Db	1893	CGCATGGGACAAATCTGACTGCCGAAGGGGTGMAAGCGCGCTGGTTTCCATGCCGCTCAC	1892							
QY	125	GGAACCTCTTGATGAGAGAGTGGATGAGTACAAAGAGAGCGTCTCCCTGCGCAGCTAC	184							
Db	1893	CGAGCGGTTGACAAAGACAGATGGCGCTTATCGGAATTCGTTACTGCCGAAAGACGTGAC	1952							
QY	185	AGCGAGATCAGCATCGAGAGCGGGGTCACTTCGCTGGCGAGAACTGTCGAGGCCA	244							
Db	1953	CGCCCGCGTGGCCGTGGAAAGGGGTATCGCTGACTTACTGGTTCCAAATACGTGGCCGTGAA	2012							
QY	245	AGCGAAGGCCATTTGGCATTCACACAAGTTCCGCGCGAGTGTCTTCGCCGGAGCATCTACAA	304							
Db	2013	CGGGCGTATGTTGGGACATGACACACTTCGGGTGATGTCGCCCGGCTGAGCAGCTGTTGCA	2072							
QY	305	GGAGTACGCATCACCGTGGAGAGCATTTGGCAATCGCCAA	346							
Db	2073	GGAGTTCCGCTTCAACGCTTATTAACGTGGTCGCTTAAAGCCAA	2114							

```

1      RESULT 9
2      US-08-311-731A-127
3      ; Sequence 127, Application US/08311731A
4      ; Patent No. 6583256
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: SMITH, DOUGLAS
8      ; APPLICANT: MAO, JEN-I
9      ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
10     ; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
11     ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
12     ; NUMBER OF SEQUENCES: 411
13     ;
14     ; CORRESPONDENCE ADDRESS:
15     ; ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.
16     ; STREET: 600 ATLANTIC AVENUE
17     ; CITY: BOSTON
18     ; STATE: MASSACHUSETTS
19     ; COUNTRY: USA
20     ; ZIP: 02210
21     ;
22     ; COMPUTER READABLE FORM:
23     ; MEDIUM TYPE: Floppy disk
24     ; COMPUTER: IBM PC compatible
25     ; OPERATING SYSTEM: PC-DOS/MS-DOS
26     ; SOFTWARE: Patentln Release #1.0, Version #1.25
27     ; CURRENT APPLICATION DATA:
28     ; APPLICATION NUMBER: US/08/311,731A
29     ; FILING DATE:
30     ; CLASSIFICATION: 530
31     ;
32     ; ATTORNEY/AGENT INFORMATION:
33     ; NAME: GATES, EDWARD R.
34     ; REGISTRATION NUMBER: 3,616
35     ; REFERENCE/DOCKET NUMBER: C0044/7125
36     ; TELECOMMUNICATION INFORMATION:
37     ; TELEPHONE: 617/720-3500
38     ; TELEFAX: 617/720-2441
39     ; INFORMATION FOR SEQ ID NO: 127:
40     ; SEQUENCE CHARACTERISTICS:
41     ; LENGTH: 35881 base pairs
42     ; TYPE: nucleic acid
43     ; STRANDEDNESS: double
44     ; TOPOLOGY: circular
45     ; MOLECULE TYPE: DNA (genomic)
46     ; HYPOTHEICAL: NO
47     ; ANTI-SENSE: NO
48     ;
49     ; ORIGINAL SOURCE:
50     ; ORGANISM: MYCOBACTERIUM LAPRAE
51     ; US-08-311-731A-127

```

```

1      RESULT 9
2      US-08-311-731A-127
3      ; Sequence 127, Application US/08311731A
4      ; Patent No. 6583256
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: SMITH, DOUGLAS
8      ; APPLICANT: MAO, JEN-I
9      ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
10     ; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
11     ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
12     ; NUMBER OF SEQUENCES: 411
13     ;
14     ; CORRESPONDENCE ADDRESS:
15     ; ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.
16     ; STREET: 600 ATLANTIC AVENUE
17     ; CITY: BOSTON
18     ; STATE: MASSACHUSETTS
19     ; COUNTRY: USA
20     ; ZIP: 02210
21     ;
22     ; COMPUTER READABLE FORM:
23     ; MEDIUM TYPE: Floppy disk
24     ; COMPUTER: IBM PC compatible
25     ; OPERATING SYSTEM: PC-DOS/MS-DOS
26     ; SOFTWARE: Patentln Release #1.0, Version #1.25
27     ; CURRENT APPLICATION DATA:
28     ; APPLICATION NUMBER: US/08/311,731A
29     ; FILING DATE:
30     ; CLASSIFICATION: 530
31     ;
32     ; ATTORNEY/AGENT INFORMATION:
33     ; NAME: GATES, EDWARD R.
34     ; REGISTRATION NUMBER: 3,616
35     ; REFERENCE/DOCKET NUMBER: C0044/7125
36     ; TELECOMMUNICATION INFORMATION:
37     ; TELEPHONE: 617/720-3500
38     ; TELEFAX: 617/720-2441
39     ; INFORMATION FOR SEQ ID NO: 127:
40     ; SEQUENCE CHARACTERISTICS:
41     ; LENGTH: 35881 base pairs
42     ; TYPE: nucleic acid
43     ; STRANDEDNESS: double
44     ; TOPOLOGY: circular
45     ; MOLECULE TYPE: DNA (genomic)
46     ; HYPOTHEICAL: NO
47     ; ANTI-SENSE: NO
48     ;
49     ; ORIGINAL SOURCE:
50     ; ORGANISM: MYCOBACTERIUM LAPRAE
51     ; US-08-311-731A-127

```

Query Match 25.7%; Score 99; DB 4; Length 35881;
Best Local Similarity 56.2%; Pred. No. 3.6e-18;
Matches 186; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 13 ACCTGACATCATTTGGGTTGGGCAACCGGCTCCGAGCTGAGATCGCGGCAATCGCGCCG 72
DB 19067 AGCTGACATCATTTGGATGCGCACCGGATCGAGGTCCAACTCGCTGTGCGAGCTCA 19126
QY 73 ACAGCTGAGAAAGGAGGAGAGACGCTCCGCTCTCTGCTTCTGCTCTCTGGAATCTCT 132
DB 19127 AGTTGTGCGGATTAAGACATCATTTGCGGGTGTGTGATGCGCTGTGTGAATGTGT 19186
QY 133 TTGATGAGAGTCGATGATGATCAAGAGAGCTCTCTCTGCGACATGACAGCGAGGA 192
DB 19187 TCGAGTCAAGCGGTACGATGATGCGAGATGTGTGCTCCCGTCAATGTGCGACGGG 19246
QY 193 TCAGCATCGAGCGCGGCTCACTCTCGGCTGGGAGAGTACGTCGAGCCCAAGGCAAG 252
DB 19247 TGGCCGTGAGCGCGCGCTCGCGCAATGCTGCAATAGCTGTGCGAGACACCGGCA 19306
QY 233 CCATTGGCATGACAAATTCGGGCGAGTCTCTCGCGGACGATCTCAAGAGTACG 312
DB 19307 TTGTGTCATCGACGCTACGCGGAAATCCGAGATTACAGACTTGTTCCTGAGTACG 19366
QY 313 GCATCACCGTGGAGAGCATTCGCACTGC 343
DB 19367 GCTTACGCGGAGCGCGGTGTGCGCAGC 19397

RESULT 10
US-09-531-266-1
Sequence 1, Application US/09531266

Patent No. 6797509
GENERAL INFORMATION:
APPLICANT: DUNICAN, L.K.
APPLICANT: MCCORMACK, ASHLING
APPLICANT: STABELTON, CLIONA
APPLICANT: BURKE, KEVIN
APPLICANT: MCKEL, BETTINA
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TAL GENE
FILE REFERENCE: MAS/21123/258100
CURRENT APPLICATION NUMBER: US/09/531,266
CURRENT FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/142,915
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 6995
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (2471)..(3550)
OTHER INFORMATION: tal-Gen
US-09-531-266-1

Query Match 24.4%; Score 93.8; DB 4; Length 6995;
Best Local Similarity 54.9%; Pred. No. 5.9e-17;
Matches 185; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

QY 15 CCTGACATCATTTGGGTTGGGCAACCGGCTCCGAGCTGAGATCGCGGCAATGCGGCCGAC 74
DB 1953 CCAGATGATCTCTCAATGGGCTCCGCTCCGAGTTCAAGTTAAGCTGCGAAG 2012
QY 75 GAGCTGAGAAAGAGGAGGAGAGCGTCCGCTGCTCTGCTCTCTCTGGAATCTTT 134
DB 2013 GCTCTGAAAGTGAAGGCGCTGCACTCGGTGTTTCTGCTCTGCAATGATGTTTC 2072
QY 135 GATGAGACATCGGATGATGATCAAGAGAGCGTCTCTGCGAGCTCAAGGAGATC 194
DB 2073 CAGGAGCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2132

QY 195 AGCATGAGCGCGGCTCCATCTCGCTGGGAGAGTACGTGAGAGCCCAAGAGGCC 254
DB 2133 TCTGTGAAGCTGGGATGCAATGCTGTGATCCGCTCTTGTGGGACCCAGGCGCTGT 2192
QY 255 ATTGACATGCAAGTTGCGCGCGAGTCTCTGCGGAGCAGATCAAGAGTACGCGC 314
DB 2193 GTCTCCTTGACACTTCTGCTGCTCTCTGCGGATTAACAGACCTCTGTTAGAAATGCGC 2252
QY 315 ATCACCGTGGAGAGCATTCATTCATTCGCACTGCAAGAGCT 351
DB 2253 ATCACCGAGATGACATGCTGTCGACGCGGCAAGAGACT 2289

RESULT 11
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match 22.3%; Score 85.8; DB 3; Length 4403765;
Best Local Similarity 53.0%; Pred. No. 1.6e-13;
Matches 183; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 2 AACCGGCAACCAAGCTGATCATTTGGTGGGCAACCGGCTCCGAGCTGAGATCGCGG 61
DB 1628319 ACCGGGCGAGAAACCGGATCTTCTATCGCACCGGCTCGAGGTGCACTGGCGGT 1628260
QY 62 CAATGCGCGCGAGCTGAGAGAGAGGAGAGAGCGTCCGCTGCTCTGCTCTC 121
DB 1628259 CGCGGCGGAGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1628200
QY 122 CTGGGAATCTTTGATGAGCACTGCGATGATGATGATGATGATGATGATGATGATGAT 181
DB 1628199 CCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1628140
QY 182 CACAGCGAGATCAAGATGAGAGCGGCTCACTCTGCGCTGCGAGAAATGATGATGATG 241
DB 1628139 GTGCGGCGGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1628080
QY 242 CCAAGGCAAGGCGATTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 301
DB 1628079 CACGGGCGGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1628020
QY 302 CAAGAGTACGAGATCAAGCGGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 346
DB 1628019 CCGGAGTACGAGTCTTCACTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1627975

RESULT 12
US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328


```
SOFTWARE: Word Perfect 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,693A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: W. Gary Goodson
REGISTRATION NUMBER: 22,387
REFERENCE/DOCKET NUMBER: Lit-PI-296
TELECOMMUNICATION INFORMATION:
TELEPHONE: (208)526-9469
TELEFAX: (208)526-8339
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 6641 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-064-693A-25

Query Match      21.5%; Score 82.8; DB 3; Length 6641;
Best Local Similarity 53.0%; Pred. No. 8,7e-14;
Matches 177; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 13 AGCTGACATCATTTGGTTGGGACCGGCTCCGAGCTGAGATCGCGGCAATGCGCCG 72
DB 3768 ACCCGAATGATTTTCATCGCTACCGGTTCAAGATGAACTGAGTGTGCTGCTACG 3827
QY 73 AGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 132
DB 3828 AAAAATGATCTCCGAAAGCGTAAAGCGCGGTGTGTCAATGTCTTACCGAGCAT 3887
QY 133 TTGATGAGAGCTCGATGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 192
DB 3888 TTGACAGAGAGATGCTGCTTACCGTAAATCCGTACTGCCAAAGCGTTACTGCA 3947
QY 193 TCAGATCAGAGCGCGGCTCACTCTCGAGTGCAGAGATCGTGCAGAGCCAGAGAG 252
DB 3948 TTGCTGTGAAGACGGGTATTTGCTGACTGATCAAGATATGTGCGCTGAAGCGT 4007
QY 253 CCATTGCGATCACAAGTTCCGCGGAGTCTCTGCGGAGAGATCTAAGAGATGAG 312
DB 4008 TCGTGTGATGACCACTTCGCGTGAATCTGCTCCGAGAGAGCTGTGTTGAAG 4067
QY 313 GCATCAGCGTGGAGAGCATTTGCAACTGCCAA 346
DB 4068 GCTTCACTGTGATTAACGTTGTTGCAAGACAA 4101

RESULT 15
US-08-961-527-49
Sequence 49, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 11443 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-49

Query Match      20.9%; Score 80.6; DB 3; Length 11443;
Best Local Similarity 51.9%; Pred. No. 4,7e-13;
Matches 182; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 17 TGACATCATTTGGTTGGGACCGGCTCCGAGCTGAGATCGCGGCAATGCGCCGAGCA 76
DB 10003 TGATCTATTTATCATTTGCTACAGAGATCTGAGGTCAATCTAGCTATCAAGCTGAAGA 10062
QY 77 GCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 136
DB 10063 ATTGCTTTTACAGGTGTAAGATGATGTGTATCTATGCTTACACCGAATTTTGA 10122
QY 137 TGAGAGTGCAGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196
DB 10123 TGCTCAAGATGCTACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10182
QY 197 CATGAGCGCGGCTCACTCTCGAGTGCAGAGATCGTGCAGAGCCAGAGAGAGCAT 256
DB 10183 CATTTAAATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10242
QY 257 TGGCATGCAAGATTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 316
DB 10243 CGTATTTACATCTTGGGTGCTCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 10302
QY 317 CACCGTGAAGAGATCATTTGCACTGCCAAGAGCTTTTAAGAGTAAAC 367
DB 10303 TACGTTAGAGATATCTGTTGCTCAAGTTAAGTCCCTATAGAACCAATTAC 10353

Search completed: May 4, 2005, 12:28:49
Job time : 126.658 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 436.803 Seconds
(without alignments)
5365.716 Million cell updates/sec

Title: US-09-300-482-356

Perfect score: 385
Sequence: 1 CAACCGGCAACCAAGCTGAC.....ACGTCGTGGAGTCTTTTTC 385

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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9:	/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
13:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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16:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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22:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	385	100.0	385	US-09-987-899-4513	Sequence 4513, Ap
2	363.2	94.3	1656	US-10-425-114-609	Sequence 609, App
3	361	93.8	1420	US-10-425-114-19700	Sequence 19700, A
4	359.4	93.4	3311	US-10-425-115-157267	Sequence 157267,
5	356.8	92.7	1686	US-10-425-114-3351	Sequence 3351, Ap
6	326.8	84.9	423	US-09-987-899-4512	Sequence 4512, Ap
7	295.2	76.7	300	US-09-987-899-4502	Sequence 4502, Ap
8	292.2	75.9	2107	US-10-767-701-14710	Sequence 14710, A
9	265	68.8	273	US-09-987-899-4499	Sequence 4499, Ap
10	249.6	64.8	276	US-09-987-899-4501	Sequence 4501, Ap
11	247.8	64.4	646	US-10-333-184-131	Sequence 131, App

12	247.8	64.4	1122	US-10-333-184-361	Sequence 361, App
13	247.6	64.3	2636	US-10-437-963-84321	Sequence 84321, A
14	247.6	64.3	630	US-10-767-701-10148	Sequence 10148, A
15	246.4	64.0	2869	US-10-739-930-5298	Sequence 5298, App
16	245	63.6	1127	US-10-333-184-156	Sequence 156, App
17	241.2	62.6	299	US-09-987-899-4504	Sequence 4504, Ap
18	232	60.3	630	US-09-910-664-118	Sequence 118, App
19	232	60.3	630	US-10-333-184-138	Sequence 138, App
20	230.4	59.8	622	US-10-333-184-139	Sequence 139, App
21	211	54.8	649	US-10-425-115-153110	Sequence 153110,
22	209.2	54.3	242	US-09-987-899-4505	Sequence 4505, Ap
23	189.4	49.2	235	US-09-987-899-4477	Sequence 4477, Ap
24	183.8	47.7	1758	US-10-260-238-9447	Sequence 5947, Ap
25	183.8	47.7	2354	US-10-437-963-88892	Sequence 88892, A
26	178.8	46.4	1146	US-10-424-599-32345	Sequence 32345, A
27	176.6	45.9	630	US-10-767-701-3173	Sequence 3173, App
28	171.6	44.6	978	US-10-425-114-9690	Sequence 9690, Ap
29	171.6	44.6	2168	US-10-425-114-9339	Sequence 9339, Ap
30	171.6	44.6	3914	US-10-424-599-96112	Sequence 96112, A
31	168.8	43.8	2594	US-10-333-184-334	Sequence 334, App
32	164.8	42.8	265	US-09-987-899-4507	Sequence 4507, Ap
33	163	42.3	1172	US-09-910-664-121	Sequence 121, App
34	163	42.3	1239	US-10-333-184-135	Sequence 135, App
35	163	42.3	1239	US-10-333-184-168	Sequence 168, App
36	162.8	42.3	693	US-10-380-935-32	Sequence 32, App1
37	161.8	42.0	15172	US-10-380-935-36	Sequence 36, App1
38	161.8	42.0	15172	US-10-380-935-36	Sequence 36, App1
39	161.4	41.9	2608	US-10-333-184-147	Sequence 147, App
40	160.8	41.8	647	US-10-333-184-129	Sequence 129, App
41	160.8	41.8	693	US-10-333-184-200	Sequence 200, App
42	155	40.3	581	US-09-770-152-150	Sequence 150, App
43	155	40.3	2226	US-09-938-842A-283	Sequence 283, App
44	155	40.3	2226	US-09-938-842A-283	Sequence 283, App
45	150.8	39.2	287	US-09-987-899-4506	Sequence 4506, Ap

ALIGNMENTS

RESULT 1
US-09-987-899-4513
Sequence 4513, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262,979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076,712
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4513
LENGTH: 385
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3078-007-Q1-X1-G3
US-09-987-899-4513

Query Match 100.0%, Score 385, DB 11, Length 385;
Best Local Similarity 100.0%, Pred. No. 1.8e-108;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 CAACGGCAACCAAGCTGACATTCATTTGAGTGGACGCGCTCGAGTGGAGATCGCGG 60
1 CAACGGCAACCAAGCTGACATTCATTTGAGTGGACGCGCTCGAGTGGAGATCGCGG 60

QY 61 GCAATGCGGCGGAGAGTGAAGAGAGGAGAGAGCGCTCCGCTGCTCTGTTGCTCT 120
|
Db 61 GCAATGCGGCGGAGAGTGAAGAGAGGAGAGAGCGCTCCGCTGCTCTGTTGCTCT 120
|
QY 121 CCTGGGAATCTTTGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGAGC 180
|
Db 121 CCTGGGAATCTTTGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGAGC 180
|
QY 181 TCACAGGAGAGATCAGCATCGAGGCCGGGTCCACTCTCGGCTGGCAGAACTACGTCGAG 240
|
Db 181 TCACAGGAGAGATCAGCATCGAGGCCGGGTCCACTCTCGGCTGGCAGAACTACGTCGAG 240
|
QY 241 CCCAAGGCAAGGCGCATTTGGCATCGACAAGTTCCGCGGAGAGTCCCTCCGCGGACCATCT 300
|
Db 241 CCCAAGGCAAGGCGCATTTGGCATCGACAAGTTCCGCGGAGAGTCCCTCCGCGGACCATCT 300
|
QY 301 ACAAGAGATACCGCATCACCGTGGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 360
|
Db 301 ACAAGAGATACCGCATCACCGTGGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 360
|
QY 361 TAACAAAGGCTCTGGAGATTTTTTT 385
|
Db 361 TAACAAAGGCTCTGGAGATTTTTTT 385
|

RESULT 2
US-10-425-114-609
; Sequence 609, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 609
; LENGTH: 1656
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700084322_FLI
US-10-425-114-609

Query Match 94.3%; Score 363.2; DB 17; Length 1656;
Best Local Similarity 96.6%; Pred. No. 1.2e-101;
Matches 371; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 CAACCGGCAACCAAGCCTGACATCATTTGGTTGGGCAACCGGCTCCGAGCTGAGATCGCG 60
|
Db 1023 CGACCGGCAACCAAGCCTGACATCATTTGATGAGGAGACCGGCTCCAGATGAGATCGCGG 1082
|
QY 61 GCATGCGGCGGAGCAGCTGAGAGAGAGAGAGAGCGGTCCGCTCGTCTCGTCTCGTCT 120
|
Db 1083 CCAAGGCGGCGGAGCAGCTGAGAGAGAGAGAGAGCGGTCCGCTCGTCTCGTCTCGTCT 1142
|
QY 121 CCTGGGAATCTTTGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGCGAGC 180
|
Db 1143 CCTGGGAATCTTTGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGCGAGC 1202
|
QY 181 TCACAGGAGAGATCAGCATCGAGGCCGGGTCCACTCTCGGCTGGCAGAACTACGTCGAG 240
|
Db 1203 TCACAGGAGAGATCAGCATCGAGGCCGGGTCCACTCTCGGCTGGCAGAACTACGTCGAG 1262
|
QY 241 CCCAAGGCAAGGCGCATTTGGCATCGACAAGTTCCGCGGAGAGTCCCTCCGCGGACCATCT 300
|
Db 241 CCCAAGGCAAGGCGCATTTGGCATCGACAAGTTCCGCGGAGAGTCCCTCCGCGGACCATCT 300
|

Db 1263 CCCAAGGCAAGGCGCATTTGGCATCGACAAGTTCCGCGGAGAGTCCCTCCGCGGACCATCT 1322
|
QY 301 ACAAGAGATACCGCATCACCGTGGAGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 360
|
Db 1323 ACAAGAGATACCGCATCACCGTGGAGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 1382
|
QY 361 TAACAAAGGCTCTGGAGATTTTTTT 384
|
Db 1383 TAACAAAGGCTCTGGAGATTTTTTT 1406
|

RESULT 3
US-10-425-114-19700
; Sequence 19700, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 19700
; LENGTH: 1420
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: L1B3150-102-F10_FLI
US-10-425-114-19700

Query Match 93.8%; Score 361; DB 17; Length 1420;
Best Local Similarity 96.1%; Pred. No. 5.5e-101;
Matches 370; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 CAACCGGCAACCAAGCCTGACATCATTTGGTTGGGCAACCGGCTCCGAGCTGAGATCGCG 60
|
Db 790 CGACCGGCAACCAAGCCTGACATCATTTGATGAGGAGACCGGCTCCGAGCTGAGATCGCGG 849
|
QY 61 GCAATGCGGCGGAGCAGCTGAGAGAGAGAGAGAGCGGTCCGCTCGTCTCGTCTCGTCT 120
|
Db 850 CCAAGGCGGCGGAGCAGCTGAGAGAGAGAGAGAGCGGTCCGCTCGTCTCGTCTCGTCT 909
|
QY 121 CCTGGGAATCTTTGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGCGAGC 180
|
Db 910 CCTGGGAATCTTTGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGCGAGC 969
|
QY 181 TCACAGGAGAGATCAGCATCGAGGCCGGGTCCACTCTCGGCTGGCAGAACTACGTCGAG 240
|
Db 970 TCACAGGAGAGATCAGCATCGAGGCCGGGTCCACTCTCGGCTGGCAGAACTACGTCGAG 1029
|
QY 241 CCCAAGGCAAGGCGCATTTGGCATCGACAAGTTCCGCGGAGAGTCCCTCCGCGGACCATCT 300
|
Db 1030 CCCAAGGCAAGGCGCATTTGGCATCGACAAGTTCCGCGGAGAGTCCCTCCGCGGACCATCT 1089
|
QY 301 ACAAGAGATACCGCATCACCGTGGAGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 360
|
Db 1090 ACAAGAGATACCGCATCACCGTGGAGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 1149
|
QY 361 TAACAAAGGCTCTGGAGATTTTTTT 385
|
Db 1150 TAACAAAGGCTCTGGAGATTTTTTT 1174
|

RESULT 4
US-10-425-115-157267
; Sequence 157267, Application US/10425115
; Publication No. US20040214272A1

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/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(5322)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 157267
/ LENGTH: 3311
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_75006C.1
US-10-425-115-157267

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Query Match          93.4%; Score 359.4; DB 18; Length 3311;
Best Local Similarity 95.8%; Pred. No. 2e-100;
Matches 369; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 CAACCGGCAACCAAGCTTGCATCATTTGGTGGCAACCGGCTCCAGCTGAGATCGCG 60
DB 2233 CGACCGGCAACCAAGCTTGCATCATTTGGTGGCAACCGGCTCCAGCTGAGATCGCG 2292
QY 61 GCAATCGGCGCCGACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 2293 CCAAGGCGCCGACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2352
QY 121 CCTGGGAACCTTTGATGAGCAGTGGATGATGATGATGATGATGATGATGATGATG 180
DB 2353 CCTGGGAACCTTTGATGAGCAGTGGATGATGATGATGATGATGATGATGATGATG 2412
QY 181 TCACAGCAGAGATCAGCATCAGAGCGGCTCCACTCTCGCTGGCAGAGTACGTGAG 240
DB 2413 TCACAGCAGAGATCAGCATCAGAGCGGCTCCACTCTCGCTGGCAGAGTACGTGAG 2472
QY 241 CCCAAGGCAAGGCGCATTTGGCATGACAGTTCCGCGCGAGTCTCTCGCGGAGCATCT 300
DB 2473 CCCAAGGCAAGGCGCATTTGGCATGACAGTTCCGCGCGAGTCTCTCGCGGAGCATCT 2532
QY 301 ACAAGAGTACCGGATCAGCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 2533 ACAAGAGTACCGGATCAGCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2592
QY 361 TAACAACGGCTCTGGAGTTTATTTT 385
DB 2593 TAACAACGGCTCTGGAGTTTATTTT 2617

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RESULT 5
US-10-425-114-3351
/ Sequence 3351, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaka, Jack E.
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 3351
/ LENGTH: 1686
/ TYPE: DNA
/ ORGANISM: Zea mays

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/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700262031_FLI
US-10-425-114-3351

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Query Match          92.7%; Score 356.8; DB 17; Length 1686;
Best Local Similarity 95.6%; Pred. No. 1.1e-99;
Matches 367; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 CAACCGGCAACCAAGCTTGCATCATTTGGTGGCAACCGGCTCCAGCTGAGATCGCG 60
DB 1119 CGACCGGCAACCAAGCTTGCATCATTTGGTGGCAACCGGCTCCAGCTGAGATCGCG 1178
QY 61 GCAATCGGCGCCGACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 1179 CCAAGGCGCCGACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1238
QY 121 CCTGGGAACCTTTGATGAGCAGTGGATGATGATGATGATGATGATGATGATGATG 180
DB 1239 CCTGGGAACCTTTGATGAGCAGTGGATGATGATGATGATGATGATGATGATGATG 1298
QY 181 TCACAGCAGAGATCAGCATCAGAGCGGCTCCACTCTCGCTGGCAGAGTACGTGAG 240
DB 1299 TCACAGCAGAGATCAGCATCAGAGCGGCTCCACTCTCGCTGGCAGAGTACGTGAG 1358
QY 241 CCCAAGGCAAGGCGCATTTGGCATGACAGTTCCGCGCGAGTCTCTCGCGGAGCATCT 300
DB 1359 CCCAAGGCAAGGCGCATTTGGCATGACAGTTCCGCGCGAGTCTCTCGCGGAGCATCT 1418
QY 301 ACAAGAGTACCGGATCAGCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 1419 ACAAGAGTACCGGATCAGCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1478
QY 361 TAACAACGGCTCTGGAGTTTATTTT 384
DB 1479 TAACAACGGCTCTGGAGTTTATTTT 1502

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RESULT 6
US-09-987-899-4512
/ Sequence 4512, Application US/09987899
/ Publication No. US20040116682A1
/ GENERAL INFORMATION:
/ APPLICANT: Cheikh, Nordine
/ APPLICANT: Liu, Jindong
/ APPLICANT: Miller, Phillip W.
/ APPLICANT: O Connell, Keith M.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
/ TITLE OF INVENTION: With the Carbon Assimilation Pathway
/ FILE REFERENCE: 16517.258
/ CURRENT APPLICATION NUMBER: US/09/987,899
/ CURRENT FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: US 09/262,979
/ PRIOR FILING DATE: 1999-03-04
/ PRIOR APPLICATION NUMBER: US 60/076,712
/ PRIOR FILING DATE: 1998-03-06
/ NUMBER OF SEQ ID NOS: 7341
/ SEQ ID NO 4512
/ LENGTH: 423
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3060-013-01-K1-A12
US-09-987-899-4512

Query Match          84.9%; Score 326.8; DB 11; Length 423;
Best Local Similarity 95.2%; Pred. No. 1.5e-90;
Matches 337; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 CAACCGGCAACCAAGCTTGCATCATTTGGTGGCAACCGGCTCCAGCTGAGATCGCG 60
DB 70 CGACCGGCAACCAAGCTTGCATCATTTGGTGGCAACCGGCTCCAGCTGAGATCGCG 129
QY 61 GCAATCGGCGCCGACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120

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Db 130 CCAAGGCCCCGAGCACTGAGAGAGAGGCGCAAGCGCTCCGCTGCTCTGCTCT 189
QY 121 CTTGGGAAGCTTTTGTATGATGACAGTGGATGATCAAGAGAGAGCTCTCTGCGCAG 180
Db 190 CTTGGGAAGCTTTTGTATGATGACAGTGGATGATCAAGAGAGAGCTCTCTGCTGCGC 249
QY 181 TCACAGGAGATGATGATGAGAGGCGGGTCCCTCTGCTGCTGCGCAAGATGATGAGAG 240
Db 250 TCACAGGAGATGATGATGAGAGGCGGGTCCCTCTGCTGCTGCGCAAGATGATGAGAG 309
QY 241 CCCAAGGCAAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 310 CCCAAGGCAAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 369
QY 301 ACAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 354
Db 370 ACAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423

RESULT 7
US-09-987-899-4502

Sequence 4502, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jingdong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262,979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076,712
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4502
LENGTH: 300
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700048347H1
US-09-987-899-4502

Query Match Best Local Similarity 76.7%; Score 295.2; DB 11; Length 300;
Matches 297; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 71 CGACGAGCTGAGGAG 130
Db 1 CGACGAGCTGAGGAG 60
QY 131 CTTTATGATGAG 190
Db 61 CTTTATGATGAG 120
QY 191 GATGAGATGAG 250
Db 121 GATGAGATGAG 180
QY 251 GGCATTGGAGATGAG 310
Db 181 GGCATTGGAGATGAG 240
QY 311 CGGAGTACCGTGGAG 370
Db 241 CGGAGTACCGTGGAG 300

RESULT 8

US-10-767-701-14710
Sequence 14710, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5353)B
CURRENT APPLICATION NUMBER: US/10/767,701
PRIOR FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 14710
LENGTH: 2107
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUST982_1
US-10-767-701-14710

Query Match Best Local Similarity 75.9%; Score 292.2; DB 18; Length 2107;
Matches 327; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 CAACGGGCAACAGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
Db 1244 CAACGGGCAACAGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1303
QY 61 GCATGCGGCGAG 120
Db 1304 AAAGGCTGCGGAG 1363
QY 121 CTTGGAACTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db 1364 CTTGGAACTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423
QY 181 TCACGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 1424 TCACGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1483
QY 241 CCCAAGGCAAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 1484 CCCAAGGCAAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
QY 301 ACAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db 1544 ACAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1603
QY 361 TAACACGCTGAGAGATTTT 385
Db 1604 TAACACGCTGAGAGATTTT 1628

RESULT 9
US-09-987-899-4499

Sequence 4499, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jingdong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262,979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076,712
NUMBER OF SEQ ID NOS: 7341

```

? SEQ ID NO 4499
? LENGTH: 273
? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
? OTHER INFORMATION: Clone ID: 700044755H1
? US-09-967-899-4499

```

Query Match	68.8%;	Score 265;	DB 11;	Length 273;
Best Local Similarity	98.2%;	Pred. No. 1.6e-71;		
Matches 268; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

QY	50	GGAATCGCGGCAATGCGGCGCGAGCTAGAAAGAGGGAAGACGCTCCGCTCGT	109
QY	1	GGAATCGCGGCAAGCGCCCGCAGACGTGAGAAAGAGGGGAGACGGTCCGCTCGT	60
QY	110	CTCGTTCGTCCTCTGGGAACTCTTTGATGAGCAGTCGATGAGTCAAGAGAGCGTCTT	169
QY	61	CTCGTTCGTCCTCTGGGAACTCTTTGATGAGCAGTCGATGAGTCAAGAGAGCGTCTT	120
QY	170	CCCTGCGCAGCGCACAAGGAGGATAGACATCGAAGCGGGGTCCACTCTGGGCTGGAGAA	229
QY	121	CCCTGCGCAGCGCACAAGGAGGATAGACATCGAAGCGGGGTCCACTCTGGGCTGGAGAA	180
QY	230	GTAAGTCGAGCCCAAGGCAAGGCCATTGGCATCGACAAATTGCGGCGCAGAGTCTCTCG	289
QY	181	GTAAGTCGAGCCCAAGGCAAGGCCATTGGCATCGACAAATTGCGGCGCAGAGTCTCTCG	240
QY	290	CGGAGCATCTACAAGAGGATACGGCATCACCGT	322
QY	241	CGGAGCATCTACAAGAGGATACGGCATCACCGT	273

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RESULT 10
US-09-987-899-4501
/ Sequence 4501, Application US/09987899
/ Publication No. US2004011682A1
/ GENERAL INFORMATION:
/ APPLICANT: Cheikh, Nordine
/ APPLICANT: Liu, Jindong
/ APPLICANT: Miller, Phillip W.
/ APPLICANT: O Connell, Keith M.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
/ TITLE OF INVENTION: With the Carbon Assimilation Pathway
/ FILE REFERENCE: 16517.258
/ CURRENT APPLICATION NUMBER: US/09/987,899
/ CURRENT FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: US 09/262,979
/ PRIOR FILING DATE: 1999-03-04
/ PRIOR APPLICATION NUMBER: US 60/076,712
/ PRIOR FILING DATE: 1998-03-06
/ NUMBER OF SEQ ID NOS: 7341
/ SEQ ID NO 4501
/ LENGTH: 276
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700027425H1
/ US-09-987-899-4501

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Query Match	64.8%	Score 249.6;	DB 11;	Length 276;
Best Local Similarity	96.4%;	Pred. No. 8.7e-67;		
Matches 266; Conservative	0;	Mismatches 9;	Indels 1;	Gaps 1;

QY	14	GCTGACATCATTTGGGTTGGGCA	CGGCTTC	CCAGCTGGAAGATCG	CGGGCAATTCGGCCGA	73
Db	1	GCTTGACATCATTTGATGGCACC	GGGCTT	CCGAGTGGAGATTCGGG	CCACAGGCCGCCGA	60
QY	74	CGAGCTGAGG-AAAGAGGGGGA	AGACGGTCCGGCTCT	CGTTCGTTCCGTTCTCT	GTGGAACTCT	132
Db	61	CGAGCTGAGGTCATAGGGGAAG	ACGCTCCGGCTCTCT	CGTTCGTTCTCTGTGGAA	CTCT	120
QY	133	TTGATGACAGTCGGATGATG	CAAGGAGAGCGCTCT	CCCTCGCCGACGT	CAACGCGAGA	192

Qy	Dy
193	122
181	122
253	122
241	122

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US-10-33-184-131
; RESULT 11
; Sequence 131, Application US/10333164
; Publication No. US2004008762A1
; GENERAL INFORMATION:
; APPLICANT: Reddy, Avutu
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Skokut, Thomas
; APPLICANT: Smith, Doug
; APPLICANT: Hu, Zihua
; APPLICANT: Ruegger, Max
; APPLICANT: Shukla, Vipula
; APPLICANT: Bauer, Teresa
; APPLICANT: Weglarz, Ted
; APPLICANT: Blaklee, Beth
; APPLICANT: Oriedo, Jeremiah
; APPLICANT: Savickas, Philip
; APPLICANT: McCreery, David
; APPLICANT: Miller, Barbara
; APPLICANT: della-Cioppa, Gregory
; TITLE OF INVENTION: Nucleic Acid Compositions Confering Dwarfism Phenotype
; FILE REFERENCE: DOM-04681
; CURRENT APPLICATION NUMBER: US/10/333,184
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/219,809
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 131
; LENGTH: 646
; TYPE: DNA
; ORGANISM: Oryza japonica
; US-10-33-184-131

```

Query Match	64.4%	Score 247.8;	DB 17;	Length 646;
Best Local Similarity	-80.2%;	Pred. No. 3.6e-66;		
Matches 291; Conservative	0;	Mismatches 72;	Indels 0;	Gaps 0;

QY	1	CAACCGGGACCAAGGCTGACATCATTTGGGTTGGGACACGGGTCTCCGACTGAGATCGCG	60
Db	170	CAATCGGACAAAGCTTACTTCACTTATGTGATGAGCACTGGCTCTGAACCTAGAAATTTCG	229
QY	61	GCAATTCGGCCGACGAGCTTGAGGAAGAGGGGAAGACGTTCCGCTGTCTGTTGCTT	120
Db	230	CCAAAGGCTGCTGATGATGTTGAGGAAGAGGGGGAAGACTGTCCGTGTCTCATTTGTTTT	289
QY	121	CCGCGGAATCTTTTATGATGACGATCGGATGATGATCAAGAGAGAGCGTCTCTCCGCGCAG	180
Db	290	GCTGGGAGTTTTTCATGATGACAGTCGCTGATGATCAAGAGAAAGTTCTCCCTGAGGCTG	349
QY	181	TCACAGCGAGATCAGATCGAAGCCGGGTCACTTCCGCTGGCAGAAATGATGTCGAG	240
Db	350	TTACTGCAAGATCGCTTGAACACAGGGTCTTACTTTGATGAGCAGAAATAGTCGGAA	409
QY	241	CCCAAGGCAAGGCCATTGGATTCGACAAAGTTCCGCGCGAGTGTCTCTCGCGGACGATC	300
Db	410	GCAAGGCAAGGCTATTGTGGATTCGACAAATTCGGTGCAGATGGCTCCTGTGAAAAGTCT	469
QY	301	ACAAAGGATGCGGCATCACCTGTGAGAGCATCATTTGCACCTGCCMAAGCTTTTAAAGC	360
Db	470	ACCAGAGATATGACATCACCGCGGAGAACTGTCATTCGCAACGCAAAAGCTCTGAAGATT	529

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QY 361 TAA 363
DB 530 CAA 532

RESULT 12
US-10-333-184-361
/ Sequence 361, Application US/10333184
/ Publication No. US20040086762A1
/ GENERAL INFORMATION:
/ APPLICANT: Reddy, Avutu
/ APPLICANT: Larrinua, Ignacio
/ APPLICANT: Skokut, Thomas
/ APPLICANT: Smith, Doug
/ APPLICANT: Hu, Zihua
/ APPLICANT: Ruegger, Max
/ APPLICANT: Shukla, Vipula
/ APPLICANT: Bauer, Teresa
/ APPLICANT: Meglarz, Ted
/ APPLICANT: Blakeslee, Beth
/ APPLICANT: Oriedo, Jeremiah
/ APPLICANT: Savickas, Philip
/ APPLICANT: McCleary, David
/ APPLICANT: Miller, Barbara
/ APPLICANT: della-Cioppa, Gregory
/ TITLE OF INVENTION: Nucleic Acid Compositions Conferring Dwarfism Phenotype
/ FILE REFERENCE: DOM-04681
/ CURRENT APPLICATION NUMBER: US/10/333,184
/ CURRENT FILING DATE: 2003-10-10
/ PRIOR APPLICATION NUMBER: 60/219,809
/ PRIOR FILING DATE: 2000-07-20
/ NUMBER OF SEQ ID NOS: 571
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 361
/ LENGTH: 1122
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-333-184-361

Query Match 64.4%; Score 247.8; DB 17; Length 1122;
Best Local Similarity 80.2%; Pred. No. 4e-66;
Matches 291; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1 CAACCGGCACCAAGCCTGACATCATTTGGGTGGGCAACCGGCTCCAGCTGGAGATCGCG 60
DB 486 CAATGCGCAACAAGCCTGACCTTCTTGTATGAGCACTGGCTCTGAAGATTGTCG 545
QY 61 GCAATGCGCGCCGACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 546 CCAAGGCTGCTGATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605
QY 121 CCGTGGAACTCTTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 606 GCTGGAGCTTTTTCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 665
QY 181 TCACAGCGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 666 TTACTGCAAGATGACGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 725
QY 241 CCCAAGGCAAGGCAATTGGCATGCAAGATTGCGCGAGAGAGAGAGAGAGAGAGAGAG 300
DB 726 GCAAGGCAAGGCAATTGGCATGCAAGATTGCGCGAGAGAGAGAGAGAGAGAGAGAG 785
QY 301 ACAAGGAGTAAGGCAATCCGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 786 ACCAGGAGTAAGGCAATCCGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 845
QY 361 TAA 363
DB 846 CAA 848
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```
RESULT 13
US-10-437-963-84321
/ Sequence 84321, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukhacov, Andrey A.
/ APPLICANT: Bardazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 84321
/ LENGTH: 2636
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_83569C.1
US-10-437-963-84321
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Query Match 64.4%; Score 247.8; DB 18; Length 2636;
Best Local Similarity 80.2%; Pred. No. 4.6e-66;
Matches 291; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
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QY 1 CAACCGGCACCAAGCCTGACATCATTTGGGTGGGCAACCGGCTCCAGCTGGAGATCGCG 60
DB 1911 CAATGCGCAACAAGCCTGACCTTCTTGTATGAGCACTGGCTCTGAAGATTGTCG 1970
QY 61 GCAATGCGCGCCGACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 1971 CCAAGGCTGCTGATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2030
QY 121 CCGTGGAACTCTTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 2031 GCTGGAGCTTTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2090
QY 181 TCACAGCGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 2091 TTACTGCAAGATGACGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2150
QY 241 CCCAAGGCAAGGCAATTGGCATGCAAGATTGCGCGAGAGAGAGAGAGAGAGAGAGAG 300
DB 2151 GCAAGGCAAGGCAATTGGCATGCAAGATTGCGCGAGAGAGAGAGAGAGAGAGAGAG 2210
QY 301 ACAAGGAGTAAGGCAATCCGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 2211 ACCAGGAGTAAGGCAATCCGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2270
QY 361 TAA 363
DB 2271 CAA 2273

RESULT 14
US-10-767-701-10148
/ Sequence 10148, Application US/10767701
/ Publication No. US20040172684A1
/ GENERAL INFORMATION:
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53535)B
```

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? CURRENT APPLICATION NUMBER: US/10/767,701
? CURRENT FILING DATE: 2004-01-29
? NUMBER OF SEQ. ID NOS: 63128
? SEQ. ID NO. 10148
? LENGTH: 630
? TYPE: DNA
? ORGANISM: Sorghum bicolor
? FEATURE:
? OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS61383_1
US-10-767-701-10148

```

Query Match	64.3%	Score 247.6;	DB 18;	Length 630;
Best Local Similarity	80.7%;	Pred. No. 4.2e-66;		
Matches 289; Conservative	0;	Mismatches 69;	Indels 0;	Gaps 0;

QY	1	CAAACGGACCAAGCCTGCATCATTTGGTTTGGGCAACCGGCTCCGACCTGGAAATCGCG	60
QY	7	CAACAGGCAACAAGCCTGATCTCATCGTGGTTGAGTACCGGCTTGAACTGAGATTTGCTG	66
QY	61	GCATTCGGCCGACGAGCTGAGAGAGAGGGGAGAACCCTCCGCGTCTCTGTTCCGCT	120
QY	67	CCAAGGCTGCTGATGATTGAGGAGAGGGGGAAGACATCCGTTGTTGATCATTTGGTTT	126
QY	121	CCTGGGAATCTTTTGATGAGCAGTCGGAATGAGTACAAAGAGAGCGTCTCTCCGCGACG	180
QY	127	CCGCGGAATTTTGGAGGAACAGTCAGACGAATACAAAGAGAGTGTTCTTCTGAGGCGG	186
QY	181	TCACAGCGAGGATCAGCATCGAGGCGGGCTCACTCTCGCTGGCAGAAATGTCGGAG	240
QY	187	TTACTGCAAGAAATCGCAATTGAGGCTGGTTTACTCTTCGATGCGAAAGTACATTGGAG	246
QY	241	CCCAAGGCAAGGCAATTTGGCATCGACAAGTTCCGGCGGAGGCTCCGCGGGACATCT	300
QY	247	CCGAGGGCAAGGCAATTTGGCATCGACAATTCGGGCAATGCTCTCTGCTGGAAAGATCT	306
QY	301	ACAAGGATGACGCGATCAACCGTGGAGACATCATTTGCAATGCGCAAGAGCTTTTAAAG	358
QY	307	ACAAGAGTATGGCATCACTGTGGAGGGGTGTTATTTCCGGCGCAACAAAGCTTTCTAAG	364

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RESULT 15
US-10-739-930-5298
; Sequence 5298, Application US/107399930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: KOVALLIC, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 5298
; LENGTH: 2869
; TYPE: DNA
; ORGANISM: Trifolium aestivum
; FEATURES:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER730_1608
; US-10-739-930-5298

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Query Match	64.0%	Score 246.4;	DB 18;	Length 2869;
Best Local Similarity	80.3%	Pred. No. 1.3e-65;		
Matches 289; Conservative	0;	Mismatches 71;	Indels 0;	Gaps 0;

QY	1	60
QY	CAACCCGCGACCAACCTGACATCATTTGGGTTTGGGACACCGGCTCCGAGTGGAGATCGGG	60
Db	CGACCGACACCAACCTGACATCATTAATGAGCAGCTGGTTTGAAGTTAGATTTGCTG	204
QY	1988	
QY	61	120
QY	GCATGGCGCGCGACGCTGAGGAAAGAGGGGGGAAAGCGTCCGCTCGTCTCCGCT	120
Db	2048	2107
QY	121	180
QY	CCTGGGAATCTTTGATGAGCAGTCCGATGAGTACAGAGAGCGCTCTCCCTGCCGAC	180

Db	2108	GCTGGGAATCTTTCAGACGACGTCAGATGATGATCAAGAGAGAGGTGCTCCCTTGAGGCCG	2167
Qy	181	TCACAGCGAGGATTCAGCATCGAGGCCGGGTCACATCTCGGCTGGCAGAGTACGTCGGAG	240
Db	2168	TCACCGCAAGATTCAGATTCGAGGCTGCTTCACCTCCGATGGCAAAATGATGTCCGAT	2227
Qy	241	CCCAAGGCAAGGCCATTGGCATCGACAAATTTGGCGCGAGTGCTCTCTCCGGGACGATCT	300
Db	2228	CCAAAGGCAAGACCATTCGGCATCGACAAATTTGGCGCGACGCTCCGCCCCGAAAGATCT	2287
Qy	301	ACAAGAGTACGGCATCACCGTGGAGAGCATCATTTGCACTGCCAAGAGCTTTTAAAGC	360
Db	2288	ACAAGAGTACGGCATCACCGCGGAGAACCTCATTCGCCGACGCCAAGAGCTTTAAATC	2347

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Job time : 437.803 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 77.2515 Seconds
(without alignments)
5591.830 Million cell updates/sec

Title: US-09-300-482-569

Perfect score: 264
Sequence: 1 ctgacttcagcagcattccca.....gacatgcttcagcatttca 264

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51.2	19.4	7218	1	US-08-232-463-14 Sequence 14, Appl
2	36.6	13.9	148794	4	US-09-949-016-12751 Sequence 12751, A
3	34.8	13.2	107820	4	US-09-792-616-1 Sequence 1, Appl
4	34.2	13.0	197336	4	US-09-949-016-12881 Sequence 12881, A
5	34.2	13.0	197337	4	US-09-949-016-14376 Sequence 14376, A
6	34.2	13.0	234288	4	US-09-949-016-17272 Sequence 17272, A
7	33	12.5	14412	4	US-09-949-016-14044 Sequence 14044, A
8	32.8	12.4	69263	4	US-09-949-016-12594 Sequence 12594, A
9	32.8	12.4	69709	4	US-09-949-016-16036 Sequence 16036, A
10	32.8	12.4	122772	4	US-09-949-016-14132 Sequence 14132, A
11	32.6	12.3	106380	4	US-09-949-016-17553 Sequence 17553, A
12	32.4	12.3	857	4	US-09-509-7128-31 Sequence 31, Appl
13	32	12.1	14205	4	US-09-949-016-2722 Sequence 2722, Ap
14	32	12.1	14205	4	US-09-949-016-14664 Sequence 14664, A
15	31.4	11.9	279	4	US-09-248-796A-7005 Sequence 7005, Ap
16	31.4	11.9	800	4	US-09-765-298A-17 Sequence 17, Appl
17	31.4	11.9	4002	3	US-09-356-952-9 Sequence 9, Appl
18	31.4	11.9	5415	4	US-09-976-594-311 Sequence 311, App
19	31.2	11.8	53526	3	US-08-658-136-2 Sequence 2, Appl
20	31.2	11.8	53577	3	US-08-658-136-1 Sequence 1, Appl
21	31	11.7	17879	4	US-09-949-016-12992 Sequence 12992, A
22	31	11.7	18474	4	US-09-949-016-17559 Sequence 17559, A
23	31	11.7	56963	4	US-09-949-016-12966 Sequence 12966, A
24	31	11.7	56968	4	US-09-949-016-11888 Sequence 11888, A
25	31	11.7	187136	4	US-09-949-016-17231 Sequence 17231, A
26	30.8	11.7	141560	4	US-09-949-016-16476 Sequence 16476, A
27	30.6	11.6	289	3	US-09-007-005-17 Sequence 17, Appl

C 28	30.6	11.6	289	3	US-09-244-796-17	Sequence 17, Appl
C 29	30.6	11.6	57726	4	US-09-949-016-16430	Sequence 16430, A
C 30	30.6	11.6	221545	4	US-09-949-016-18875	Sequence 18875, A
C 31	30.4	11.5	304533	4	US-09-949-016-15371	Sequence 15371, A
C 32	30.4	11.5	304533	4	US-09-949-016-15372	Sequence 15372, A
C 33	30.4	11.5	390416	4	US-09-949-016-16923	Sequence 16923, A
C 34	30.2	11.4	601	4	US-09-949-016-201472	Sequence 201472, A
C 35	30.2	11.4	601	4	US-09-949-016-201473	Sequence 201473, A
C 36	30.2	11.4	58782	4	US-09-949-016-16851	Sequence 16851, A
C 37	30.2	11.4	86639	4	US-09-949-016-17397	Sequence 17397, A
C 38	30	11.4	690	4	US-09-248-796A-1546	Sequence 1546, Ap
C 39	30	11.4	16924	4	US-09-949-016-13720	Sequence 13720, A
C 40	30	11.4	100877	4	US-09-949-016-13276	Sequence 13276, A
C 41	30	11.4	294836	3	US-09-949-016-15974	Sequence 15974, A
C 42	29.8	11.3	1798	3	US-08-687-691B-1	Sequence 1, Appl
C 43	29.8	11.3	9409	4	US-09-949-016-17121	Sequence 17121, A
C 44	29.8	11.3	12222	4	US-09-949-016-12238	Sequence 12238, A
C 45	29.8	11.3	12223	4	US-09-949-016-14119	Sequence 14119, A

ALIGNMENTS

RESULT 1
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHRIFFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304772/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 883-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZ9PT-F15
US-08-232-463-14
Query Match 19.4%; Score 51.2; DB 1; Length 7218;


```

RESULT 5
US-09-949-016-14376
: Sequence 14376, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: FILE REFERENCE: CLO01307
: CURRENT APPLICATION NUMBER: US/09/949, 016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14376
: LENGTH: 197337
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(197337)
: OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14376

Query Match      13.0%; Score 34.2; DB 4; Length 197337;
Best Local Similarity 52.4%; Pred. No. 1.7;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY      73  AAGCGCTTGGCCCCGAGATTCTGCGTCTCACCTTCAAACTTTTCATCGCTTTA 132
Db      14519 AGTGTGCCAGGCCCTGGGAGGCTTCGTGCTCTCTCTCTCCCTTCCCTCCCTTC 14578

QY      133  ATCAAAACTTAACTTATCCGCTTCCCTCCGATTCATTCATCGTCCCTCTTAAACCT 192
Db      14579 CTCCTGCACTCTCTCCCTCCCTCTCTCCATCCCTCCCTCCCTGCGCCCTCC 14638

QY      193  CCTTACGATCAATATGCTCCCA 215
Db      14639 CCTCTGCAAGATGGCTGGCCA 14661

RESULT 6
US-09-949-016-17272
: Sequence 17272, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: FILE REFERENCE: CLO01307
: CURRENT APPLICATION NUMBER: US/09/949, 016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 17272
: LENGTH: 234288
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
: NAME/KEY: misc_feature

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; LOCATION: (1) ... (234288)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-17272

Query Match      13.0%; Score 34.2; DB 4; Length 234288;
Best Local Similarity 52.4%; Pred. No. 1.8;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

OY 73 AAGGCTTGCCCCGAGATTCTGGCTTCCTCCTCATTCAACCTTCTTCATGCGTTTAA 132
Db 14519 AGTGCCAGGAGCCCTGGAGAGGCTCTGGCTCTCTCTCCCTTCCTCCCTCCCTTC 14578

OY 133 ATCAACAACATCACTATCCGCTTCCCTCCGATCATCATCAGTCCGCTCCCTTAACCT 192
Db 14579 CTCTGTGACATCTCCCTCCCTCTCTCTCTCCATCCCTCTCCCTCCCTCTGCGCTTC 14638

OY 193 CCTTACGGATCAAAATGCTCCCA 215
Db 14639 CCTCTGTGACATGAGTGGTGGCA 14661

RESULT 7
US-09-949-016-14044/c
Sequence 14044, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14044
LENGTH: 4412
TYPE: DNA
ORGANISM: Human
US-09-949-016-14044

Query Match      12.5%; Score 33; DB 4; Length 4412;
Best Local Similarity 54.5%; Pred. No. 0.59;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

OY 78 CTGCGCCCCGAGATTCGTGGCTTCCTCAACCTTCTTCATGCGCTTTATATAC 137
Db 335 CTCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 276

OY 138 AAAACTACATCATCGCTTCCCTCGATCATCATCAGTCCCTCTTAAACCTTCCTTA 197
Db 275 CTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 216

OY 198 C 198
Db 215 C 215

RESULT 8
US-09-949-016-12594/c
Sequence 12594, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016

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;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 12594
;; LENGTH: 69263
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)---(69263)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12594

Query Match 12.4%; Score 32.8; DB 4; Length 69263;
Best Local Similarity 54.0%; Pred. No. 3;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 115 CTTCTTCATCGCTTTTATACAAACTAACCTATCCGCTTCCGATCCATTCACCT 174
DB 59885 CTGCTTCAGTGTCTAATAACATTAAGAGAACCAACCGCTTAATTAAATTCACCAAT 59826
QY 175 CGCTCCCTCTTAAACCTCTTACGATCAATGCTCCCAACAGATGGAAATGGAAGTC 234
DB 59825 CTCTACTCCCTTAATATCTTCTCAGAGATACTTAAACAATTTCTTGATAGATGTT 59766
QY 235 CTGC 238
DB 59765 CTTC 59762

RESULT 9
US-09-949-016-16036/c
; Sequence 16036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16036
; LENGTH: 69709
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)---(69709)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16036

Query Match 12.4%; Score 32.8; DB 4; Length 69709;
Best Local Similarity 54.0%; Pred. No. 3;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 115 CTTCTTCATCGCTTTTATACAAACTAACCTATCCGCTTCCGATCCATTCACCT 174
DB 59885 CTGCTTCAGTGTCTAATAACATTAAGAGAACCAACCGCTTAATTAAATTCACCAAT 59826

QY 175 CGCTCCCTCTTAAACCTCTTACGATCAATGCTCCCAACAGATGGGAATGGAAGTC 234
DB 59825 CTCTACTCCCTTAATATCTTCTCAGAGATACTTAAACAATTTCTTGATAGATGTT 59766
QY 235 CTGC 238
DB 59765 CTTC 59762

RESULT 10
US-09-949-016-14132/c
; Sequence 14132, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14132
; LENGTH: 122772
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14132

Query Match 12.4%; Score 32.8; DB 4; Length 122772;
Best Local Similarity 59.8%; Pred. No. 4.1;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 16 TCCCAATGCGCTTCGTTTCCAGCTTCACGCCAATTCAGCTTCTTATCAGAG 75
DB 78404 TCACAAATGCGCTTGAATTTGGACCCAGAACCTCAATTCATCTCTGCTCCAT 78345
QY 76 CGCTTGCGCCCGGAGATTCGCTTCTCACC 107
DB 78344 GGCACCCCTCAATATCTTACTTCTCTCACC 78313

RESULT 11
US-09-949-016-17553/c
; Sequence 17553, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17553
; LENGTH: 106380
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17553

Query Match 12.3%; Score 32.6; DB 4; Length 106380;

Best Local Similarity 58.9%; Pred. No. 4.5;
Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 137 CAAACTACCTATCCGCTCCCTCCGATTCATTCAGTCCCTCTTAAACCTCTT 196
Db 28232 CAAACCTAACCACTATCTACTATCTTCCATTCCTTCATACGCTCTTCCCTCCG 28173

QY 197 ACGATCAATGCTCCCAACAGATGGAAATGGAA 231
Db 28172 ATGATCTGATGCTCTCCATATACATTCCTGCA 28138

RESULT 12
US-09-509-712B-31/c

; Sequence 31, Application US/09509712B
; Patent No. 6777177

; GENERAL INFORMATION:
; APPLICANT: Rubin, Donald H.

; APPLICANT: Organ, Edward L.

; TITLE OF INVENTION: Mammalian Genes Involved in Viral

; FILE REFERENCE: 01123.0004

; CURRENT APPLICATION NUMBER: US/09/509,712B

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: PCT/US98/21276

; PRIOR FILING DATE: 1998-10-08

; PRIOR APPLICATION NUMBER: 60/062,021

; PRIOR FILING DATE: 1997-10-10

; NUMBER OF SEQ ID NOS: 127

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 31

; LENGTH: 857

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:
; NAME/KEY: misc.feature

; LOCATION: 1- 857

; OTHER INFORMATION: n = g, a, c or t (u)

US-09-509-712B-31

Query Match 12.3%; Score 32.4; DB 4; Length 857;
Best Local Similarity 47.5%; Pred. No. 0.41;
Matches 66; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 62 TTCCTATCAGAGGCTTGGCCCGAGATTCCTGCTTCCTCACTTCAAACTTCTTC 121

Db 248 TTGCATGATGACATCNCATCTTTCGANGTCTGTGTTCCCAACCCNATGATGCTTC 189

QY 122 CATCGCTTTTATATCAAAACTTACCTTTCGCTTCCCTCGATCCATTCAGTCCGCTCC 181

Db 188 TTTTCGTTTGGCNCATCCCAACNTTTCCTTANTCCNCCGACCCGTTCTGTTNC 129

QY 182 TCTTAAACCTCTTACCG 200

Db 128 NCCGAAATTTTTCG 110

RESULT 13
US-09-949-016-2722

; Sequence 2722, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2722

; LENGTH: 4082

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-2722

Query Match 12.1%; Score 32; DB 4; Length 4082;
Best Local Similarity 50.7%; Pred. No. 1.3;
Matches 77; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 26 TTCGTTTCAAGCTCTTACAGCCAAATTCAGTCTTCTTATACAGAGCGCTTGGCC 85

Db 118 TCCGGGTCCTCCGCGCCACCTATTCAGCTCTCTCTTCCGATTCCTCTGCTC 177

QY 86 CCGAATTCGCTTCCGATTCAGCTTCAAACTTCTTCAATGCTTTTATACAAACTTAA 145

Db 178 ACCCATCTCTCTCCGCGCCCTTCTGATTCCTCAACCGCTCTGATTCCTCTCCG 237

QY 146 CCTATCCGCTTCCCTCCGATTCATTCAGTCCG 177

Db 238 CTTTCCAGAGACCCAGACCCCTGACCC 269

RESULT 14
US-09-949-016-14464

; Sequence 14464, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14464

; LENGTH: 14205

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14464

Query Match 12.1%; Score 32; DB 4; Length 14205;
Best Local Similarity 50.7%; Pred. No. 2.5;
Matches 77; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 26 TTCGTTTCAAGCTCTTACAGCCAAATTCAGTCTTCTTATACAGAGCGCTTGGCC 85

Db 2118 TCCGGGTCCTCCGCGCCACCTATTCAGCTCTCTCTTCCGATTCCTCTGCTC 2177

QY 86 CCGAATTCGCTTCCGATTCAGCTTCAAACTTCTTCAATGCTTTTATACAAACTTAA 145

Db 2178 ACCCATCTCTCTCCGCGCCCTTCTGATTCCTCAACCGCTCTGATTCCTCTCCG 2237

QY 146 CCTATCCGCTTCCCTCCGATTCATTCAGTCCG 177

Db 2238 CTTTCCAGAGACCCAGACCCCTGACCC 2269

RESULT 15

US-09-248-796A-7005/c

; Sequence 7005, Application US/09248796A

; Patent No. 6747137

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; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 7005
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-7005

Query Match      11.9%; Score 31.4; DB 4; Length 279;
Best Local Similarity 48.6%; Pred. No. 0.51;
Matches 86; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY      22  TGGCTTCGCTTCCAGCTCTCAAGCCAAATCCACTGCTTCTTATCAGAAGCGCTTC 81
      204  TCGATTCCTCTCTCTCTTTCCTCTTTCCTCTTTCCTCTCTCTCCGTCCTCCCT 145
QY      82  GCCCCGAGATTCTGCTTCCCTTCCACTTCAACCTTTCATCGCTTTATCACAAAA 141
      144  TTCTCTCTCTTCTTCTCTCTCTCTCCAGTTCCTCCCTTTTCCCTCCCTCTCTTC 85
DB      142  CTAACCTATCCGCTTCCCTCCGATCCATTCACCTGCTCCCTCTTAAACCTCTTAC 198
      84  CTCTCTCTACTTTTCCCTCTTTTTCAGCTCTCTCTCTTGTTCCTCCCTCCCTTTC 28

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 299.522 Seconds
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Title: US-09-300-482-569

Perfect score: 264
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
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12:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
13:	/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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19:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	252	95.5	747	17	US-10-424-599-43249
2	215.8	81.7	1926	17	US-10-424-599-43247
3	196.8	74.5	592	17	US-10-424-599-43245
4	145	54.9	676	17	US-10-424-599-43250
5	100.6	38.1	346	17	US-10-424-599-10015
6	100.4	38.0	305	17	US-10-424-599-65148
7	96.8	36.7	322	17	US-10-424-599-33477
8	95	36.0	376	17	US-10-424-599-132643
9	83.6	31.7	169	17	US-10-424-599-41040
10	60.4	22.9	205	17	US-10-424-599-86542
11	58.2	22.0	289	17	US-10-424-599-28474

12	52.8	20.0	208	17	US-10-424-599-58838	Sequence 58838, A
13	47.6	18.0	603	18	US-10-021-323-1453	Sequence 1453, Ap
14	45.6	17.3	183	17	US-10-424-599-15721	Sequence 15721, A
15	44.2	16.7	320	17	US-10-424-599-102259	Sequence 102259, A
16	35.2	13.3	366	18	US-10-674-124A-15571	Sequence 15571, A
17	35.2	13.3	2000	9	US-09-938-842A-3388	Sequence 3388, Ap
18	35.2	13.3	2000	11	US-09-938-842A-3388	Sequence 3388, Ap
19	34.8	13.2	7329	17	US-10-221-714A-396	Sequence 396, App
20	34.8	13.2	57181	19	US-10-741-600-17781	Sequence 17781, A
21	34.8	13.2	107820	10	US-09-792-616-1	Sequence 1, Appli
22	34.8	13.2	107820	18	US-10-764-328-1	Sequence 1, Appli
23	34.8	13.2	172984	19	US-10-484-577-661	Sequence 661, App
24	34.6	13.1	3673778	16	US-10-312-841-2	Sequence 2, Appli
25	34.4	13.0	2672	9	US-09-775-938A-34	Sequence 34, Appli
26	34.2	13.0	263852	18	US-10-812-232-6	Sequence 6, Appli
27	34.2	13.0	276820	17	US-10-271-416-9	Sequence 9, Appli
28	34	12.9	31724	13	US-10-087-192-766	Sequence 766, App
29	34	12.9	53222	18	US-10-331-053-76	Sequence 76, Appli
30	33.6	12.7	341	18	US-10-674-124A-12122	Sequence 12122, A
31	33.4	12.7	630	17	US-10-388-934-381	Sequence 381, App
32	33.2	12.6	5647	15	US-10-311-455-1540	Sequence 1540, Ap
33	33.2	12.6	6547	17	US-10-221-613-282	Sequence 282, App
34	33.2	12.6	6531	15	US-10-311-455-613	Sequence 613, App
35	33	12.5	9007	17	US-10-221-714A-337	Sequence 337, App
36	32.8	12.4	308	17	US-10-424-599-9496	Sequence 9496, Ap
37	32.8	12.4	468	17	US-10-424-599-79082	Sequence 79082, A
38	32.8	12.4	969	18	US-10-363-345A-1397	Sequence 1397, Ap
39	32.8	12.4	969	18	US-10-363-345A-1398	Sequence 1398, Ap
40	32.8	12.4	969	19	US-10-363-483A-1397	Sequence 1397, Ap
41	32.8	12.4	969	19	US-10-363-483A-1398	Sequence 1398, Ap
42	32.6	12.3	650	13	US-10-027-632-216903	Sequence 216903, A
43	32.6	12.3	650	17	US-10-027-632-216903	Sequence 216903, A
44	32.6	12.3	2074	17	US-10-425-114-5140	Sequence 5140, Ap
45	32.6	12.3	2327	17	US-10-424-599-121972	Sequence 121972, A

ALIGNMENTS

RESULT 1
US-10-424-599-43249
Sequence 43249, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 43249
LENGTH: 747
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(747)
FEATURE:
OTHER INFORMATION: unsure at all n locations
US-10-424-599-43249
Query Match 95.5%; Score 252; DB 17; Length 747;
Best Local Similarity 99.6%; Pred. No. 4.8e-72;
Matches 263; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Db 116 TCACCTGCAGCAATCCCAATGCTTCCTTCACAGCTTCACAGCCAAATCCTTC 61
OY 2 TCACCTGCAGCAATCCCAATGCTTCCTTCACAGCTTCACAGCCAAATCCTTC 61
116 TCACCTGCAGCAATCCCAATGCTTCCTTCACAGCTTCACAGCCAAATCCTTC 175

```
QY      62  TTCCTTACAGAAAGCGCTTGGCCCCCGAGATTGCTTCTCTCACTTCAAACTTCTTC 121
      176  TTCCTTACAGAAAGCGCTTGGCCCCCGAGATTGCTTCTCTCTCACTTCAAACTTCTTC 235
QY      122  CATGCGCTTTTAAATCAAAAATACTAATCGATCGCTTCCCTCGATCCATTGACCTGCTGCC 181
      236  CATGCGCTTTTAAATCAAAAATACTAATCGATCGCTTCCCTCGATCCATTGACCTGCTGCC 235
QY      182  TCTTAAAACTCTCTTACGAGATCAAAATGCTCCCAAAAGATGGAAATGGAAGTCTGCAAA 241
      296  TCTTAAAACTCTCTTACGAGATCAAAATGCTCCCAAAAGATGGAAATGGAAGTCTGCAAA 355
Db      242  GAGGACA-TGCTTCATGATCTTTA 264
      356  GAGGACAGTGTCTTCATGATCTTTA 379
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RESULT 2
US-10-424-599-43247
; Sequence 43247, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 43247
LENGTH: 1926
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_139050C.1
US-10-424-599-43247

Query Match
Best Local Similarity 81.7%; Score 215.8; DB 17; Length 1926;
Matches 237; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

```
QY      11  GCAATTCCTCAATGCTTCGCTTCCAAAGCTCTCAAGCCCAATCCACTGCTTCTATAC 70
      81  GCAATTCCTCAATGCTTCGCTTCCAAAGCTCTCAAGCCCAATCCACTGCTTCTATAC 140
QY      71  AGAAGCGCTTGGCCCCCGAGATTGCTTCTCTCACTTCAAACTTCTTCATGCTTT 130
      141  AGAAGCGCTTGGCCCCCGAGATTGCTTCTCTCTCTCAATCTTCTTCAAGCTAT 200
Db      131  TAATACAAAATACTAATCGATCGCTTCCCTCGATCCATTGACCTGCTTTAAAC 190
      201  TAATACAAAATACTAATCGATCGCTTCCCTCGATCCATTGACCTGCTTTAAAC 260
QY      191  CTCCTTACGAGATCAAAATGCTCCCAAAAGATGGAAATGGAAGTCTGCAAAAGACA-T 249
      261  CTCCTTACGAGATCAAAATGCTCCCAAAAGATGGAAATGGAAGTCTGCAAAAGACA-GT 320
QY      250  GCTTCATGATCTTTA 264
      321  GCTTCATGATCTTTA 335
Db
```

RESULT 3
US-10-424-599-43245

; Sequence 43245, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K

```
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(53223) B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 43245  
LENGTH: 592  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(592)  
OTHER INFORMATION: unsure at all n locations  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT_MRT3847_139049C.1  
US-10-424-599-43245
```

Query Match
Best Local Similarity 74.5%; Score 196.8; DB 17; Length 592;
Matches 213; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

```
QY      2  TGACTTGACGAATTCCTCAATGCTTCGCTTCCAAAGCTCTCAAGCCCAATCCACTGCTTC 61
      10  TGACTTGACGAATTCCTCAATGCTTCGCTTCCAAAGCTCTCAAGCCCAATCCACTGCTTC 69
QY      62  TTCCTTACAGAAAGCGCTTGGCCCCCGAGATTGCTTCTCTCTCACTTCAAACTTCTTC 121
      70  TTCCTTACAGAAAGCGCTTGGCCCCCGAGATTGCTTCTCTCTCACTTCAAACTTCTTC 129
Db      122  CATGCTTTTAAATCAAAAATACTAATCGATCGCTTCCCTCGATCCATTGACCTGCTGCC 181
      130  CATGCTTTTAAATCAAAAATACTAATCGATCGCTTCCCTCGATCCATTGACCTGCTGCC 189
QY      182  TCTTAAAACTCTCTTACGAGATCAAAATGCTCCCAAAAGATGGAAATGGAAGTCTGCAAA 241
      190  TCTTAAAACTCTCTTACGAGATCAAAATGCTCCCAAAAGATGGAAATGGAAGTCTGCAAA 249
Db
```

RESULT 4
US-10-424-599-43250

; Sequence 43250, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 43250
LENGTH: 676
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(676)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_139053C.1
US-10-424-599-43250

Query Match
Best Local Similarity 54.9%; Score 145; DB 17; Length 676;
Matches 154; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 31 TTTCAGGCTCTCAAGCCCAATCCACTGCTTCTCTTACAGAAAGCGCTTGGCCCCGAG 90

Db 4 TTTTCAAGCTCTCAAGGCATCTCCAGCTTCCTTATCAGAGGCTTGGCCGAG 63
QY 91 ATTCTGCTCTCTCACTTCAAACTTCTTCATGCTTTTATCAAACTAATCTAT 150
Db 64 ATTCTGCTCTCTCTCTCAATCTCTTCAAGCGCTTTATTAACAAATTAACCTCT 123
QY 151 CGGCTTCCCTCGATTCATCTGCTGCTCTTAAACCTTACG 199
Db 124 CCGCTTCCCTCGATTCATCTGCTCTCTTAAACCTTGGCG 172

RESULT 5
US-10-424-599-10015

; Sequence 10015, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 10015
; LENGTH: 346
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_109053C.1
US-10-424-599-10015

Query Match 38.1%; Score 100.6; DB 17; Length 346;
Best Local Similarity 68.5%; Pred. No. 1.5e-22;
Matches 139; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 46 CGCAATTCAGCTTCTTATCAAGAGCGCTTGGCCCGAGATTCCTCTCTCA 105
Db 3 CTCCTCAACAAATGTTCTCACTTACCAAAACCGTACGCTCAAAATTAATGCTCT 62
QY 106 CTTTCAACCTTCTTCACTGCTTTTATCAAACTAATCTGCTCTCTCCAT 165
Db 63 GGGCAATTCCTCTGAGCGCTACTCTTACAAATCATCTATCCGATTAACCTGTGAT 122
QY 166 CCATTCAGCTGCTCCCTCTTAAACCTCTTAAGGATCAAAATGCTCCGAAGATGGA 225
Db 123 TCATACACTGCTGCTCTCTTAAACCTTCACTGGAACAAATGCTCTTAAACGATGCA 182
QY 226 ATGAAGTCTCTCAAAAGAGACA 248
Db 183 ATGTAAGTCTCTGACATGATGACA 205

RESULT 6
US-10-424-599-69148

; Sequence 69148, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 69148
; LENGTH: 305

; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(305)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13453C.1
US-10-424-599-69148

Query Match 38.0%; Score 100.4; DB 17; Length 305;
Best Local Similarity 72.3%; Pred. No. 1.7e-22;
Matches 107; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 2 TCACCTTGACGCAATTCCTTCCAGTCTTCCAGCTCTCAAGCCAAATCTTGC 61
Db 158 TNNVTNACGCTATTCNANNTGNNNTCCNTNCCANGCNNNNNAACNCAATCNATTN 217
QY 62 TTCCTTATCAGAAAGGCTTGGCCCGAGATTCTGCTTCTCACTTCAAACTTCTTC 121
Db 218 TNCGGATCANAGGCGCTGNGCCNCGAGNTTNTGTGTCTCACTTCAAACTTCTTC 277
QY 122 CATCGCTTTTATCAAACTAATCTA 149
Db 278 CATCGCTTTTATCACTAATCTA 305

RESULT 7
US-10-424-599-33477

; Sequence 33477, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 33477
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_130233C.1
US-10-424-599-33477

Query Match 36.7%; Score 96.8; DB 17; Length 322;
Best Local Similarity 84.0%; Pred. No. 2.6e-21;
Matches 121; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 122 CATCGCTTTTATCAAACTAATCTAATCTGCTTCCCTCGATCATCTGCTGCC 181
Db 1 CAACACTATTAATTAAGAAATTAACCTCTCGGTTCCCTCAATTCATTCCTCTCC 60
QY 182 TCTTAAACCTCTTACGATCAATGCTCCCAACAGATGGGAATGGAAGTCTGCAAA 241
Db 61 TCTTAAACCTCTTACGATCAATGCTCCCAACAGATGGAATGGAAGTCTGCAAA 120
QY 242 GAGGAC-ATGCTTCAATGATCTTTA 264
Db 121 CAGGACAACTTCAATGATCTTTA 144

RESULT 8
US-10-424-599-132643

; Sequence 132643, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 132643
LENGTH: 376
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_90784C.1
US-10-424-599-132643

Query Match 36.0%; Score 95; DB 17; Length 376;
Best Local Similarity 67.6%; Pred. No. 1.1e-20;
Matches 148; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

QY 2. ATGGCTTCGCTTCCAAAGCTTCAAGCCCAATCCACTTCTTATCAGAGCGCTT 80
DB : ATGGCTTCATTTTCAGCTCTCAAGCCCATCTACAGCTGCTTCTTATCAGAGCGCTT 60
QY 81. CGCCCCGAGATTCGCTTCTCACCTTCAACCTTCTTCATGCTTTTATCAGAA 140
DB 61. CCGAAGAAAGAAAAG-GACACCATATATCCCCCTATGACCAAGTGTGAAGTACCA 119
QY 141. ACTAATCTATCGCTTCTTCCGATCCATTCAGTGCCTCTTAAACCTCTTACCG 200
DB 120. ACGGACTATTCATTCATTCCTACAGACCATTCCTCCCTCGTGTATCTGCAATGCG 179
QY 201. ATCAATGCTCCCAACAGATGGAGATGGAATGCTGCA 239
DB 180. AACAAATGCTCCGTCACATTTGCGACGAGATGACTTACA 218

RESULT 9
US-10-424-599-41040
Sequence 41040, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 41040
LENGTH: 169
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_13705C.1
US-10-424-599-41040

Query Match 31.7%; Score 83.6; DB 17; Length 169;
Best Local Similarity 87.7%; Pred. No. 4.4e-17;
Matches 114; Conservative 0; Mismatches 14; Indels 2; Gaps 2;
QY 136. ACAAACCTAATCCGCTTCCCTCCGATCCATTCAGTGCCTCTTAAACCTCCT 195
DB 9. ACAAAAGGAACCTCCGCTTCCCTCCGATCCATTCAGTGCCTCTTAAACCTCCTC 68
QY 196. TAC-GGATCAATGCTCCCAACAGATGGAGATGGAAGTCTCTGAAAGAGACA-TGCTT 253
DB 69. TCGGGGATCAATGCTCCCAATCAGATGGAGATGGAGTGTCTGCAAGAGAGACAGTCTT 128

QY 254. CATGATCTTT 263
DB 129. CAGGCTCTTT 138

RESULT 10
US-10-424-599-86542
Sequence 86542, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 86542
LENGTH: 205
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_49159C.1
US-10-424-599-86542

Query Match 22.9%; Score 60.4; DB 17; Length 205;
Best Local Similarity 91.5%; Pred. No. 1.9e-09;
Matches 75; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 182. TCTTAAACCTCTTACGATCAATGCTCCCAACAGATGGAGATGGAAGTCTGCAAA 241
DB 1. TCTGAAAGCTCTTGGCGATCAATGCTCCCAACAGATGGAGATGGAAGTCTGCAAA 60
QY 242. GAGGACA-TGCTTATGATCTT 262
DB 61. GAGGACGCGCTTCAATGATCTT 82

RESULT 11
US-10-424-599-28474
Sequence 28474, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 28474
LENGTH: 289
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_125713C.1
US-10-424-599-28474

Query Match 22.0%; Score 58.2; DB 17; Length 289;
Best Local Similarity 89.2%; Pred. No. 1.1e-08;
Matches 74; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY 182. TCTTAAACCTCTTACGATCAATGCTCCCAACAGATGGAGATGGAAGTCTGCAAA 241
DB 1. TCTTAAACCTATTTGCGATCAATGCTCCCAACAGATGGAGATGGAAGTCTGCAAG 60
QY 242. GAGGACA-TGCTTATGATCTT 263


```

; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_63357C.1
US-10-424-599-102259

```

```

Query Match      16.7%; Score 44.2; DB 17; Length 320;
Best Local Similarity 75.3%; Pred. No. 0.00045;
Matches 55; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```

```

QY      176 GCTCCCTCTTAAACCTCTTACGATCAATGCTCCCAACAGATGGAGATGAGTCC 235
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db       1 GCTACACGTTCAATCTTAAATATGTTCAATGCTTCCAAACAGATGGAGATGAGTCC 235
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      236 TGCAGAAGAGACA 248
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db       61 TGTATAGCTGACA 73
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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Search completed: May 4, 2005, 21:11:51
Job time : 303.522 secs

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1	91	269	4	US-09-313-294A-2271	Sequence 2271, App
2	74	1550	4	US-09-902-540-5815	Sequence 5815, App
3	74	24.7	4	US-09-902-540-1273	Sequence 1273, App
4	33.6	1200	4	US-09-134-000C-2307	Sequence 2307, App
5	33.2	601	4	US-09-949-016-163328	Sequence 163223, App
6	33.2	11.1	4	US-09-949-016-163328	Sequence 163138, App
7	33	11.0	4	US-09-949-016-167970	Sequence 167970, App
8	33	11.0	4	US-09-949-016-12881	Sequence 12881, App
9	33	11.0	4	US-09-949-016-13716	Sequence 14376, App
10	33	11.0	4	US-09-949-016-176212	Sequence 17272, App
11	32.6	601	4	US-09-949-016-176815	Sequence 176915, App
12	32.6	10.9	4	US-09-949-016-11868	Sequence 11868, App
13	32.6	10.9	4	US-09-949-016-14588	Sequence 14588, App
14	32.6	10.9	4	US-09-949-016-14589	Sequence 14589, App
15	32.6	10.9	4	US-09-949-016-17119	Sequence 17119, App
16	32.4	543	4	US-08-956-171E-931	Sequence 931, App
17	32.4	10.8	4	US-08-781-986A-931	Sequence 931, App
18	32.4	265038	4	US-09-949-016-150776	Sequence 15779, App
19	32.2	10.7	4	US-09-949-016-200077	Sequence 200076, App
20	32.2	10.7	4	US-09-621-976-2813	Sequence 2813, App
21	31.6	10.5	4	US-09-134-000C-2814	Sequence 2814, App
22	31.4	10.5	4	US-09-543-681A-3764	Sequence 3764, App
23	31.4	10.5	4	US-09-484-970B-60	Sequence 60, App
24	31	10.3	4	US-09-949-016-200077	Sequence 200077, App
25	31	84296	4	US-09-949-016-17335	Sequence 17335, App
26	30.8	531	4	US-09-621-976-1177	Sequence 1177, App
27	30.8	579	3	US-09-026-017-1	Sequence 1, App

28	30.8	10.3	579	3	US-09-631-547-1	Sequence 1, Appl. 1
29	30.8	10.3	601	4	US-09-949-016-140812	Sequence 1, Appl. 1
30	30.8	10.3	264358	4	US-09-949-016-157575	Sequence 157575, A
31	30.6	10.2	1051	3	US-08-961-083-125	Sequence 125, Appl. 1
32	30.6	10.2	1051	4	US-09-536-784-125	Sequence 125, Appl. 1
33	30.6	10.2	13206	4	US-08-961-577-33	Sequence 33, Appl. 1
34	30.6	10.2	22243	4	US-08-956-171E-164	Sequence 164, Appl. 1
35	30.6	10.2	22243	4	US-08-781-986A-164	Sequence 164, Appl. 1
36	30.6	10.1	601	4	US-09-949-016-63183	Sequence 63183, A
37	30.4	10.1	38229	4	US-09-949-016-12378	Sequence 12378, A
38	30.4	10.1	38229	4	US-09-949-016-15350	Sequence 15350, A
39	30.2	10.1	93930	4	US-09-949-016-12461	Sequence 12461, A
40	30.2	10.1	93930	4	US-09-949-016-16853	Sequence 16853, A
41	30.2	10.1	235064	4	US-09-949-016-15330	Sequence 15330, A
42	30.2	10.1	238815	4	US-09-949-016-16274	Sequence 16274, A
43	30	10.0	601	4	US-09-949-016-63182	Sequence 63182, A
44	30	10.0	24841	4	US-09-949-016-14009	Sequence 14009, A
45	30	10.0	36546	4	US-09-949-016-17543	Sequence 17543, A

ALIGNMENTS

```

RESULT 1
US-09-313-294A-2271
; Sequence 2271, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; NUMBER OF FILING DATE: 1999-05-14
; SOFTWARE: PERL Program
; SEQ ID NO 2271
; LENGTH: 269
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700552402H1
; NAME/KEY: unsure
; LOCATION: 199, 202, 205, 208, 230-231, 236, 240, 244, 248, 253, 256, 259, 267
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-2271

Query Match          30.3%; Score 91; DB 4; Length 269;
Best Local Similarity 88.2%; Pred. No. 7,1e-22;
Matches 105; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY      1 GATTATTGACACACCGAGTCTCTCGGATTGATCATCAATTGCTCACTAGACCTG 60
Db      124 GATTATTGACACACAGATCCTGCTGGATTGATCATCAATTGCTCACTAGACCTG 183

QY      61 AACGGCAACTACTCTTGTAATTGTGCAATTTCTTAAGAGGGGAGGCACACTGAAACCCGC 119
Db      184 AACGGCAACTACTCTGTAATGTAATGCAATTTCTTAAGAGGGGAGGCACCNNTAACCCGCC 241

RESULT 2
US-09-902-540-5815
; Sequence 5815, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE:38-10(15849)B

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; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5815
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5815

Query Match      24.7%; Score 74; DB 4; Length 1590;
Best Local Similarity 53.0%; Pred. No. 1.9e-15;
Matches 158; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 3 TTTATTGACAAACCCGATCTCTGGATGATCATCAAAATTGCTCAAGACCTGAA 62
DB 439 TTCTTCGACAAACGAGCCGCGACGGCTTCGACCGCTGCGCAACTGGCGGAGCGG 498
QY 63 CTGGCAACTACTCTGTTGTAATTTCTTAAGAGCGGAGCACACCTGAACCCGCAAT 122
DB 499 CTGTCGAGAGCGCTCACCCCTGCTATCAGCAAGTCGGGTGGCAACGAGAGCGGCAC 558
QY 123 GGTCTACTAGAGTACAGAAAGCCTTCAGAGATCGGGGCTGCATTTCTGAAACAGGGT 182
DB 559 GGCATGCTGAGAGCGGACCGCGGCTACTCGGCGCGGCGCTGACTTCAGCAAGACGCC 618
QY 183 GTTGCAATTAATCAAGAAATTTCTGTTGGAGTAACAGCTGTAAGATAGAGGATGTTA 242
DB 619 GTGGCCGTCACCGGCGCGGACGAGCTGACACACGCGAAGAGAGGCGTGGCTG 678
QY 243 GCTCGGTTTCTATGTTTGAATGGTGTGTGATGAGACTTCAAGAAATGCTGCTGTG 300
DB 679 CGCGCCTTCCCATGTGGAGACTGGTGGCGGCGGACGTCGTGTAATCTCCGCGGTG 736

RESULT 3
US-09-902-540-1273/c
; Sequence 1273; Application US/09902540
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1273
; LENGTH: 72704
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72704)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1273

Query Match      24.7%; Score 74; DB 4; Length 72704;
Best Local Similarity 53.0%; Pred. No. 1.5e-14;
Matches 158; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 3 TTTATTGACAAACCCGATCTCTGGATGATCATCAAAATTGCTCAAGACCTGAA 62
DB 33865 TTCTTCGACAAACGAGCCGCGGAGCTTCGACCGCTGCGCAACTGGCGGAGCGG 33806
QY 63 CTGGCAACTACTCTTGTATTTGTAATTTCTTAAGAGCGGAGCACACCTGAACCCGCAAT 122
DB 33805 CTGTCGAGAGCGCTCACCCCTGCTATCAGCAAGTCGGGTGGCAACGAGAGCGGCAC 33746
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QY 123 GGTCTACTAGAGTACAGAAAGCCTTCAGAGATGGGGGCTGCAATTCGAAACAGGT 182
DB 33745 GGCATGCTGAGAGCCGAGCGCGGCTACTCTGCGCGGCGGCTGACTTCAGACAGCGCC 33686
QY 183 GTTGCAATTAATCAAGAAATTTCTGTTGATTAACACTGCTAGAAATAGAGGATGTTA 242
DB 33685 GTGGCCGTCACCGGCGCGGACGAGCTGACAAACGCGAAGAGAGGCTGGCTG 33626
QY 243 GCTCGGTTTCTATGTTTGAATGGTGTGTGATGAGACTTCAAGAAATGCTGCTGTG 300
DB 33625 CGCGCCTTCCCATGTGGAGACTGGTGGCGGCGGACGTCGTGTAATCTCCGCGGTG 33568

RESULT 4
US-09-134-000C-2307/c
; Sequence 2307; Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2307
; LENGTH: 1200
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2307

Query Match      11.2%; Score 33.6; DB 4; Length 1200;
Best Local Similarity 56.2%; Pred. No. 0.28;
Matches 63; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 126 CTACTAGAGTACAGAAAGCCTTCAGAGATCGGGGCTGCAATTCGAAACAGGTGTT 185
DB 301 CTAACACTAGTAATGCAATATTAATTAAGACATAGAGATCGCATCGCCCAACAGGGGAA 242
QY 186 GCAATTAATCAAGAAATTTCTGTTGATTAACACTGCTGAATAGAGGAT 237
DB 241 TTTTCTCTCAAGGCGTTTCACCATGATTAAGCAAAATTAATAGAAAT 190

RESULT 5
US-09-949-016-163223/c
; Sequence 163223; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163223
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-163223
```

Query Match 11.1%; Score 33.2; DB 4; Length 601;
Best Local Similarity 56.4%; Pred. No. 0.26;
Matches 62; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 112 AACCCGCAATGCTTACTAGAGTACAGAAAGCTTCAGAGATGCGGGCTGCATTCT 171
DB 580 AAGCCAGCAATGTGCAAAAAGCAAAACAGAAAGCTGTATATAGATGAGTGCAGACTATA 521

QY 172 CGAAACAGGCTGTGCAATTAATCAAGAAATTCCTGTGGATTAACACT 221
DB 520 CGCAACAGCTGTATATATTCTTACAGCAATATCCACTGTATCAATTAATCTCT 471

RESULT 6

US-09-949-016-16318/C
Sequence 16318, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CL001307
METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 16318

LENGTH: 80004

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(80004)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-16318

Query Match 11.1%; Score 33.2; DB 4; Length 80004;
Best Local Similarity 56.4%; Pred. No. 3.9;

Matches 62; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 112 AACCCGCAATGCTTACTAGAGTACAGAAAGCTTCAGAGATGCGGGCTGCATTCT 171
DB 13605 AAGCCAGCAATGTGCAAAAAGCAAAACAGAAAGCTGTATATAGATGAGTGCAGACTATA 13546

QY 172 CGAAACAGGCTGTGCAATTAATCAAGAAATTCCTGTGGATTAACACT 221
DB 13545 CGCAACAGCTGTATATATTCTTACAGCAATATCCACTGTATCAATTAATCTCT 13496

RESULT 7

US-09-949-016-16790/C
Sequence 16790, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CL001307
METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 16790

LENGTH: 78630

TYPE: DNA

ORGANISM: Human

US-09-949-016-16790

Query Match 11.0%; Score 33; DB 4; Length 78630;
Best Local Similarity 57.1%; Pred. No. 4.5;

Matches 60; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 125 TCTACTAGAGTACAGAAAGCTTCAGAGATGCGGGCTGCATTCTCGAAACAGGTCT 184
DB 51895 TCTACTAGAGTACAGAAAGCTTCAGAGATGCGGGCTGCATTCTCGAAACAGGTCT 184

QY 185 TCGAATTAATCAAGAAATTCCTGTGGATTAACACTGCTAGAAAT 229
DB 51835 TCGAATTAATCAAGAAATTCCTGTGGATTAACACTGCTAGAAAT 229

US-09-949-016-12881
Sequence 12881, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CL001307
METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12881

LENGTH: 197336

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(197336)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12881
Query Match 11.0%; Score 33; DB 4; Length 197336;
Best Local Similarity 53.5%; Pred. No. 7.5;

Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 95 GAGCGGAGGACACCTGAAAGCCGCAATGCTTACTAGAGTACAGAAAGCTTCAGAGA 154
DB 89818 GGGCGGCTCTGGCGCCGACCCCGCAATGTTTATTGACTGTACAGAGGCTTCAGAA 89877

QY 155 TCGCGGCTGCAATTCGAAACAGGCTGTGCAATTAATCAAGAAATTCCTGTGGA 214
DB 89878 TCTTGAATGCTACACTTAAATAACAGAGGTTCAATGAAATTCATTTCAATTCCT 89937

QY 215 TTAACACTGC 223
DB 89938 TCAAGAGC 89946

RESULT 9

US-09-949-016-14376
Sequence 14376, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;;
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;;
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 14376
;; LENGTH: 197337
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(197337)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14376

Query Match 11.0%; Score 33; DB 4; Length 197337;
Best Local Similarity 53.5%; Pred. No. 7.5;
Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 95 GAGCGAGGACACACTGAAACCCGCAATGGTCTACTAGAGTACAGAAAGCCTTCAGAGA 154

DB 89818 GGGCGGCTCGCGCCGCCACCCCGCAATGTTTATTGACTCGTCAACGGCTTCAGAAA 89877

QY 155 TGGCGGGCTGCATTTCTCGAAGACAGGGTGTTCGAATTAATCAAGAAATTTCTGTGGA 214

DB 89878 TGTGAGTGTACACTTAATAATCAGAGGTTTCACATGAATAATTCATATTTCACTTCT 89937

QY 215 TAACACTGC 223

DB 89938 TCAGAGGC 89946

RESULT 10
US-09-949-016-17272
; Sequence 17272, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17272
; LENGTH: 234288
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(234288)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17272

Query Match 11.0%; Score 33; DB 4; Length 234288;
Best Local Similarity 53.5%; Pred. No. 8.2;
Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 95 GAGCGAGGACACACTGAAACCCGCAATGGTCTACTAGAGTACAGAAAGCCTTCAGAGA 154

DB 89818 GGGCGGCTCGCGCCGCCACCCCGCAATGTTTATTGACTCGTCAACGGCTTCAGAAA 89877
QY 155 TGGCGGGCTGCATTTCTCGAAGACAGGGTGTTCGAATTAATCAAGAAATTTCTGTGGA 214
DB 89878 TGTGAGTGTACACTTAATAATCAGAGGTTTCACATGAATAATTCATATTTCACTTCT 89937
QY 215 TAACACTGC 223
DB 89938 TCAGAGGC 89946

RESULT 11
US-09-949-016-176915/c
; Sequence 176915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176915
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-176915

Query Match 10.9%; Score 32.6; DB 4; Length 601;
Best Local Similarity 56.2%; Pred. No. 0.43;
Matches 59; Conservative 1; Mismatches 45; Indels 0; Gaps 0;

QY 125 TCTACTAGAGTACAGAAAGCCTTCAGAGATGCGGGCTGCATTTCTCGAAGACGGGCT 184

DB 369 TCTACTAATAATACAAAATTAATGACGACATGTGCGACGACCTGAGCTTGACGAGC 310

QY 185 TGCATTAATCTAAGAAATTTCTGTGGATTAACATGCTAGAAAT 229

DB 309 TGAGATTAYGCCACTGCACCTCAACCTGGGTGACAGCAAGAACT 265

RESULT 12
US-09-949-016-11868
; Sequence 11868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11868
; LENGTH: 300598
; TYPE: DNA
; ORGANISM: Human

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(300598)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11868

Query Match
Best Local Similarity 10.9%; Score 32.6; DB 4; Length 300598;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 69 ACTACTCTTGTAATGTCTATTTCTAAGACGGAGCAGACCTGAAACCCGCAATGCTCTA 128
DB 49305 ATTCCTTTTCCATGCTGCTTACTAAGCTCACTATCATCAGAAAGCCCTTGAGACATG 49364
QY 129 CTAGAAGTACAGAAAGCCTTCAGAGATGCGGGGCTGCAATTCCTCGAAACAGGGTGTGCA 188
DB 49365 TTACAAATACATATATGCTCCAGCTCCTCCGACATCTCGAAAAATGCTGCTCCA 49424
QY 189 ATTACTCAAGAAAT 203
DB 49425 CCAACTTCATTAAGAT 49439

RESULT 13
US-09-949-016-14588
Sequence 14588, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14588
LENGTH: 302604
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(302604)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14588

Query Match
Best Local Similarity 10.9%; Score 32.6; DB 4; Length 302604;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 69 ACTACTCTTGTAATGTCTATTTCTAAGACGGAGCAGACCTGAAACCCGCAATGCTCTA 128
DB 99311 ATTCCTTTTCCATGCTGCTTACTAAGCTCACTATCATCAGAAAGCCCTTGAGACATG 99370
QY 129 CTAGAAGTACAGAAAGCCTTCAGAGATGCGGGGCTGCAATTCCTCGAAACAGGGTGTGCA 188
DB 99371 TTACAAATACATATATGCTCCAGCTCCTCCGACATCTCGAAAAATGCTGCTCCA 99430
QY 189 ATTACTCAAGAAAT 203
DB 99431 CCAACTTCATTAAGAT 99445

RESULT 14
US-09-949-016-14589
Sequence 14589, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14589
LENGTH: 302604
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(302604)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14589

Query Match
Best Local Similarity 10.9%; Score 32.6; DB 4; Length 302604;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 69 ACTACTCTTGTAATGTCTATTTCTAAGACGGAGCAGACCTGAAACCCGCAATGCTCTA 128
DB 99311 ATTCCTTTTCCATGCTGCTTACTAAGCTCACTATCATCAGAAAGCCCTTGAGACATG 99370
QY 129 CTAGAAGTACAGAAAGCCTTCAGAGATGCGGGGCTGCAATTCCTCGAAACAGGGTGTGCA 188
DB 99371 TTACAAATACATATATGCTCCAGCTCCTCCGACATCTCGAAAAATGCTGCTCCA 99430
QY 189 ATTACTCAAGAAAT 203
DB 99431 CCAACTTCATTAAGAT 99445

RESULT 15
US-09-949-016-17119

Sequence 17119, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17119
LENGTH: 308362
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(308362)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17119

Query Match
Best Local Similarity 10.9%; Score 32.6; DB 4; Length 308362;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Matches	72;	Conservative	0;	Mismatches	64;	Indels	0;	Gaps	0;
QY	69	ACTACTCTGTAATGTCATTTCTTAAGACGGAGGCACACTGAAACCGCATGTGCTTA	128						
Db	99127	ATTCCTTTCCCTATGGTGCTTACTTAAGCTCACTTATCATCAGAAATGCCCTAGAGCATG	99186						
QY	129	CTGAAGTACAGAAAGCCTTCAGAGATGCGGGGCTCAATTTCGAAACAGGGTGTTCGA	188						
Db	99187	TTTAAAAATACATATAGGCTTCCGAGCTCTTCCCTGACATCCGAAAAATTCCTGCTCCA	99246						
QY	189	ATTACTCAGAAAAAT	203						
Db	99247	CCAACTTCATTAAGAT	99261						

Search completed: May 4, 2005, 12:28:56
Job time : 91.7858 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 340.366 Seconds
(without alignments)
5365.716 Million cell updates/sec

Title: US-09-300-482-619

Perfect score: 300
Sequence: 1 gattattatgacacacccgat.....ttcagaatgctgctgrrg 300

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	300	100.0	300	10	US-09-237-183A-276	Sequence 276, App
2	296.8	98.9	2175	17	US-10-425-114-33220	Sequence 33220, A
3	288.8	96.3	2737	18	US-10-425-115-79832	Sequence 79832, A
4	285.6	95.2	1822	17	US-10-425-114-2691	Sequence 2691, App
5	285.6	95.2	3088	17	US-10-425-114-35572	Sequence 35572, A
6	285.6	95.2	3830	18	US-10-425-115-79836	Sequence 79836, A
7	247.2	82.4	1937	18	US-10-437-963-92448	Sequence 92448, A
8	244	81.3	2696	18	US-10-739-930-5223	Sequence 5223, App
9	242.4	80.8	2666	18	US-10-437-963-92447	Sequence 92447, A
10	225.2	75.1	423	18	US-10-767-701-27794	Sequence 27794, A
11	218.4	72.8	1491	18	US-10-767-795-1472	Sequence 1472, App

12	208.8	69.6	1411	17	US-10-425-114-9307	Sequence 9307, App
13	208.8	69.6	2218	17	US-10-425-114-29640	Sequence 29640, A
14	208.8	69.6	2547	17	US-10-425-114-11100	Sequence 11100, A
15	197.6	65.9	1836	9	US-09-938-842A-1222	Sequence 1222, App
16	197.6	65.9	1836	11	US-09-938-842A-1222	Sequence 1222, App
17	159.8	53.3	235	10	US-09-237-183A-285	Sequence 285, App
18	149.2	49.7	1327	18	US-10-767-701-13572	Sequence 13572, A
19	145	48.3	248	10	US-09-237-183A-282	Sequence 282, App
20	138.4	46.1	243	10	US-09-237-183A-284	Sequence 284, App
21	136.4	45.5	234	10	US-09-237-183A-2168	Sequence 2168, App
22	131.8	43.9	296	10	US-09-237-183A-286	Sequence 286, App
23	124	41.3	304	10	US-09-237-183A-288	Sequence 288, App
24	110	36.7	288	10	US-09-237-183A-283	Sequence 283, App
25	110	36.7	1374	17	US-10-425-114-2651	Sequence 2651, App
26	107.6	35.9	1575	17	US-10-369-493-43763	Sequence 43763, A
27	96.6	32.2	260	18	US-10-437-963-92859	Sequence 92859, A
28	96.4	32.1	1551	17	US-10-369-493-33584	Sequence 33584, A
29	95.4	31.8	228	10	US-09-237-183A-287	Sequence 287, App
30	95.2	31.7	223	10	US-09-237-183A-2170	Sequence 2170, App
31	92	30.7	218	10	US-09-237-183A-2171	Sequence 2171, App
32	83.6	27.9	1251	17	US-10-369-493-42789	Sequence 42789, A
33	82.4	27.5	267	10	US-09-237-183A-278	Sequence 278, App
34	76	25.3	258	10	US-09-237-183A-279	Sequence 279, App
35	74	24.7	1542	17	US-10-369-493-43239	Sequence 43239, A
36	64	21.3	1596	17	US-10-369-493-26424	Sequence 26424, A
37	57.6	19.2	423	18	US-10-425-115-158321	Sequence 158321, A
38	52.6	17.5	362	10	US-09-237-183A-2182	Sequence 2182, App
39	52.4	17.5	1557	17	US-10-369-493-44626	Sequence 44626, A
40	38.2	12.7	205	10	US-09-237-183A-2169	Sequence 2169, App
41	36.2	12.1	1608	17	US-10-282-122A-40331	Sequence 40331, A
42	34.2	11.4	241	17	US-10-424-599-83869	Sequence 83869, A
43	34	11.3	579	9	US-09-815-242-8232	Sequence 8232, App
44	33	11.0	276820	17	US-10-271-416-9	Sequence 9, Appl
45	32.8	10.9	711	14	US-10-001-254-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-09-237-183A-276
; Sequence 276, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21 (15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; PRIOR FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 276
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-276

Query Match 100.0%; Score 300; DB 10; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.1e-89;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATTATTGACAAACCCGATCTGCTGGGATTCATCAATTCCTCAACTAGACCGG 60
DB 1 GATTATTGACAAACCCGATCTGCTGGGATTCATCAATTCCTCAACTAGACCGG 60
QY 61 AACTGCAACTACTCTTGTATTCATTTCAAGAGCGAGCAACCTGAAACCGCA 120
DB 61 AACTGCAACTACTCTTGTATTCATTTCAAGAGCGAGCAACCTGAAACCGCA 120

QY	12	ATGCTCTACAGAAATGACAGAAAGCCTTACAGATGCGGCGCTGCATTTCTCGAAACAG	180
Db	121	ATGCTCTACAGAAATGACAGAAAGCCTTACAGATGCGGCGCTGCATTTCTCGAAACAG	180
QY	181	GTTGTGCATTAATCTCAAGAAATTCCTCGTTGGATTAACATCTGTAGAAATGAGGAGTGT	240
Db	181	GTTGTGCATTAATCTCAAGAAATTCCTCGTTGGATTAACATCTGTAGAAATGAGGAGTGT	240
QY	241	TAGCTCGTTTCCTATGTTGATTTGGATGGGTGGGTGAGGACCTTCAGAAATGTCTGTGTG	300
Db	241	TAGCTCGTTTCCTATGTTGATTTGGATGGGTGGGTGAGGACCTTCAGAAATGTCTGTGTG	300

RESULT 2
ITS-10-43

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US-10-425-114-33220      : Sequence 33220      Application US/10425114
: Publication NO. US20040034888A1
: GENERAL INFORMATION:
: APPLICANT: Liu, Jindong
: APPLICANT: Zhou, Yihua
: APPLICANT: Kovalic, David K.
: APPLICANT: Screen, Steven E
: APPLICANT: Tabaska, Jack E
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(5313)B
: CURRENT APPLICATION NUMBER: US/10/425,114
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 33220
: LENGTH: 2175
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Clone ID: UC-ZMFLMO1707A12_FLI
: US-10-425-114-33220

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Query Match	98.9%;	Score 296.8;	DB 17;	Length 2175;
Best Local Similarity	99.3%;	Score 307.5;	DB 17;	Length 2175;

Matches 298; Conservatively 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	GATTATTATGACAAACCGATCTCTGGATGATCATCAAAATTTGCTCAACTAGGACCTG	60
QY	768	GATTTATTGACAACAACCGATCTCTGGATGATCATCAAAATTTGCTCAACTAGGACCTG	827
QY	61	AACGGCAACACTCTTGTATATGTCAATTTCTAAGCGGAGGACACACTGAAACCGCA	120
QY	828	AACGGCAACACTCTTGTATATGTCAATTTCTAAGCGGAGGACACACTGAAACCGCA	887
QY	121	ATGCTCTACTGAAAGTACAGAAAGCCTTCAGAGATCGGGGCTGCATTTCTGAAACAG	180
QY	888	ATGCTCTACTGAAAGTACAGAAAGCCTTCAGAGATCGGGGCTGCATTTCTGAAACAG	947
QY	181	GTGTGCAATTAATCTCAAGAAATTTCTCTGTGGATTAACCTCTGTGAATAGAGGGATGT	240
QY	948	GTGTGCAATTAATCTCAAGAAATTTCTCTGTGGATTAACCTCTGTGAATAGAGGGATGT	1007
QY	241	TAGTCGGTTCCTCAATGTTGATTTGGGTGGGTGATGACCTTCAGAAATGTCGTGCTGG	300
QY	1008	TAGTCGGTTCCTCAATGTTGATTTGGGTGGGTGATGACCTTCAGAAATGTCGTGCTGG	1067

RESULT 3
IS-10-42

Sequence 79832, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

```

, TITLE OF INVENTION: Plants
, FILE REFERENCE: 38-21(53222)B
, CURRENT APPLICATION NUMBER: US/10/425,115
, CURRENT FILING DATE: 2003-04-28
, NUMBER OF SEQ ID NOS: 369326
, SEQ ID NO 79832
, LENGTH: 2737
, TYPE: DNA
, ORGANISM: Zea mays
, FEATURE:
, OTHER INFORMATION: clone ID: MFT4577_172832C.1
, US-10-425-115-79832

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Query Match
Rest Local

	Query Match	Best Local Similarity	Matches	Conservative	0;	Mismatches	7;	Indels	0;	Gaps	0;
QY	1	GATTATATGCAACCCGATCTCTGCTGGATGTATCATCAAAATGCTCACTAGACCTG	60								
Db	1181	GATTATATGCAACCCGATCTCTGCTGGATGTATCATCAAAATGCTCACTAGACCTG	1240								
QY	61	AACCTGGCACTACTCTTGTAATGTCAATTTCTAAGACGGAGGACACCTGAACCCGCA	120								
Db	1241	AACCTGGCACTACTCTTGTAATGTCAATTTCTAAGACGGAGGACACCTGAACCCGCA	1300								
QY	121	ATGCTCACTAGAAAGTACAGAAAAGCTTTCAGAATGCGGGCTGCAATTTCTGAAACAG	180								
Db	1301	ATGCTCACTAGAAAGTACAGAAAAGCTTTCAGAATGCGGGCTGCAATTTCTGAAACAG	1360								
QY	181	GTGTTGCAATTACTCAAGAAATTTCTGTGTGATTAACACTGTGTAGAATGAGGATG	240								
Db	1361	GTGTTGCAATTACTCAAGAAATTTCTGTGTGATTAACACTGTGTAGAATGAGGATG	1420								
QY	241	TAGCTGGATTCCTATGTTTGATTTGGGATGTGTGTAGACTTCAGAAATGCTCTGTGG	300								
Db	1421	TAGCTGGATTCCTATGTTTGATTTGGGATGTGTGTAGACTTCAGAAATGCTCTGTGG	1480								

RESULT 4

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US-10-425-114-2691
Sequence 2691, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 2691
LENGTH: 1822
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700221523_FLI
US-10-425-114-2691

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Query Match	Score	DB	Length
95.2%	285.6	17	1822
Best Local Similarity	97.0%	2	3204

Matches 291; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 GATTATTATGCAACACCGATCCGCTGGGATGATCATCAATTGCTCAATGAGCCGTG 60
2b GATTATTATGCAACACGATCCGCTGGGATGATCATCAATTGCTCAATGAGCCGTG 60
430 GATTATTATGCAACACGATCCGCTGGGATGATCATCAATTGCTCAATGAGCCGTG 489
61 AATGGGAATTAATCTTGTAATGTCATTTCTAAGCGGAGGCAACCTGAACCCGCA 120

Db 490 AACTGCACTACTCTTGTATGTCATTTCTAAGAGCGAGGACACCTGAAACCCGCA 549
Qy 121 ATGGCTTACTAAGACAGAAAGCCTTCAAGATGCGGGGCTGCAATTCGAAACAG 180
Db 550 ATGGGCTACTGAAAGACAGAAAGCCTTCAAGATGCGGGGCTGCAATTCGAAACAG 609
Qy 181 GTGTGCAATTAAGCAAAATTCCTGTGATTAACACTGCTAGATAGAGGATGCT 240
Db 610 GTGTGCAATTAAGCAAAATTCCTGTGATTAACACTGCTAGATAGAGGATGCT 669
Qy 241 TAGCTCGGTTTCCTATGTTGATTTGGGTTGGTGAAGACTTCAGAAATGCTGCTGG 300
Db 670 TAGCTCGGTTTCCTATGTTGATTTGGGTTGGTGAAGACTTCAGAAATGCTGCTGG 729

RESULT 5
US-10-425-114-35572
; Sequence 35572, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 35572
; LENGTH: 3088
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROB73058A09_FLI
US-10-425-114-35572

Query Match 95.2%; Score 285.6; DB 17; Length 3088;
Best Local Similarity 97.0%; Pred. No. 4,3e-84;
Matches 291; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 GATTTATTGACAACACCGATCCTGCTGGAGTTGATCATCAAAATGCTCACTAGACCTG 60
Db 712 GATTTATTGACAACACCGATCCTGCTGGAGTTGATCATCAAAATGCTCACTAGACCTG 771
Qy 61 AACTGCACTACTCTTGTATGTCATTTCTAAGAGCGAGGACACCTGAAACCCGCA 120
Db 772 AACTGCACTACTCTTGTATGTCATTTCTAAGAGCGAGGACACCTGAAACCCGCA 831
Qy 121 ATGGCTTACTAAGACAGAAAGCCTTCAAGATGCGGGGCTGCAATTCGAAACAG 180
Db 832 ATGGGCTACTGAAAGACAGAAAGCCTTCAAGATGCGGGGCTGCAATTCGAAACAG 891
Qy 181 GTGTGCAATTAAGCAAAATTCCTGTGATTAACACTGCTAGATAGAGGATGCT 240
Db 892 GTGTGCAATTAAGCAAAATTCCTGTGATTAACACTGCTAGATAGAGGATGCT 951
Qy 241 TAGCTCGGTTTCCTATGTTGATTTGGGTTGGTGAAGACTTCAGAAATGCTGCTGG 300
Db 952 TAGCTCGGTTTCCTATGTTGATTTGGGTTGGTGAAGACTTCAGAAATGCTGCTGG 1011

RESULT 6
US-10-425-115-79836
; Sequence 79836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 79836
; LENGTH: 3830
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_172836C.1
US-10-425-115-79836

Query Match 95.2%; Score 285.6; DB 18; Length 3830;
Best Local Similarity 97.0%; Pred. No. 4,8e-84;
Matches 291; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 GATTTATTGACAACACCGATCCTGCTGGAGTTGATCATCAAAATGCTCACTAGACCTG 60
Db 1452 GATTTATTGACAACACCGATCCTGCTGGAGTTGATCATCAAAATGCTCACTAGACCTG 1511
Qy 61 AACTGCACTACTCTTGTATGTCATTTCTAAGAGCGAGGACACCTGAAACCCGCA 120
Db 1512 AACTGCACTACTCTTGTATGTCATTTCTAAGAGCGAGGACACCTGAAACCCGCA 1571
Qy 121 ATGGCTTACTAAGACAGAAAGCCTTCAAGATGCGGGGCTGCAATTCGAAACAG 180
Db 1572 ATGGGCTACTGAAAGACAGAAAGCCTTCAAGATGCGGGGCTGCAATTCGAAACAG 1631
Qy 181 GTGTGCAATTAAGCAAAATTCCTGTGATTAACACTGCTAGATAGAGGATGCT 240
Db 1632 GTGTGCAATTAAGCAAAATTCCTGTGATTAACACTGCTAGATAGAGGATGCT 1691
Qy 241 TAGCTCGGTTTCCTATGTTGATTTGGGTTGGTGAAGACTTCAGAAATGCTGCTGG 300
Db 1692 TAGCTCGGTTTCCTATGTTGATTTGGGTTGGTGAAGACTTCAGAAATGCTGCTGG 1751

RESULT 7
US-10-437-963-92448/C
; Sequence 92448, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boudazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 92448
; LENGTH: 1937
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_90929C.1
US-10-437-963-92448

Query Match 82.4%; Score 247.2; DB 18; Length 1937;
Best Local Similarity 89.0%; Pred. No. 2,2e-71;
Matches 267; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
Qy 1 GATTTATTGACAACACCGATCCTGCTGGAGTTGATCATCAAAATGCTCACTAGACCTG 60
Db 1 GATTTATTGACAACACCGATCCTGCTGGAGTTGATCATCAAAATGCTCACTAGACCTG 60

Db 1139 GATTATTGACAACACTGATCTGCTGGAATGACCATCAATTTGCTCACTAGACAG 1080
QY 61 AACTGGCACTACTCTTGTATTTGTCAATTTCTTAAGCGGAGGCAACCTGAAACCCGCA 120
Db 1079 AGGTTGATCTACTCTTGTATTTGTATTTCTTAAGGTGAGGACACCTGAAACCCGGA 1020
QY 121 ATGGCTACTAGAAAGTACAGAAAGCCTTCAGAGATCGGGGGCTGCATTTCTGAAACAG 180
Db 1019 ATGGCTGCTGTAAGTGCAGAAAGCCTTCGAGATCTGGGGCTGCATTTCTCGAAACAG 960
QY 181 GTGTTCGAATTAATCAAGAAATTTCTGTGTGATTAACATCTGTAGAAATAGAGGATGT 240
Db 959 GAGTTGCACTTACTCAAGAAATTTCTGTGTGATTAACATCTGTAGAAATAGAGGATGT 900
QY 241 TAGCTCGGTTTCTTATTTGATTTGGTTGGTGTGATGATTCAGAAATGTCTGCTGTG 300
Db 899 TAGCTGATTTTCCCATGTTTGAATGAGGTTGGTGAAGAACATCAAGAAATGTGAGCTGTG 840

RESULT 8
US-10-739-930-5223
; Sequence 5223, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 5223
; LENGTH: 2696
; TYPE: DNA
; ORGANISM: *Triticum aestivum*
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER6893_1
US-10-739-930-5223

Query Match 81.3%; Score 244; DB 18; Length 2696;
Best Local Similarity 88.3%; Pred. No. 36-70; Indels 0; Gaps 0;
Matches 265; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 GATTATTGACAACACCGATCTGCTGGATTCATCAATTTGCTCACTAGACCTG 60
Db 1083 GATTATTGACAACACCGATCTGCTGGATTCATCAATTTGCTCACTAGACCTG 1142
QY 61 AACTGGCACTACTCTTGTATTTGTCAATTTCTTAAGCGGAGGCAACCTGAAACCCGCA 120
Db 1143 AACTGAAATCTACTCTTGTATTTGTCAATTTCTTAAGCGGAGGCAACCTGAAACCCGCA 1202
QY 121 ATGGCTACTAGAAAGTACAGAAAGCCTTCAGAGATCGGGGGCTGCATTTCTGAAACAG 180
Db 1203 ATGGCTACTAGAAAGTACAGAAAGCCTTCAGAGATCGGGGGCTGCATTTCTGAAACAG 1262
QY 181 GTGTTCGAATTAATCAAGAAATTTCTGTGTGATTAACATCTGTAGAAATAGAGGATGT 240
Db 1263 GTGTTCGAATTAATCAAGAAATTTCTGTGTGATTAACATCTGTAGAAATAGAGGATGT 1322
QY 241 TAGCTCGGTTTCTTATTTGATTTGGTTGGTGTGATGATTCAGAAATGTCTGCTGTG 300
Db 1323 TAGATCGATTTCTTATTTGATTTGGTTGGTGTGATGATTCAGAAATGTCTGCTGTG 1382

RESULT 9
US-10-437-963-92447/c
; Sequence 92447, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(533221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 92447
; LENGTH: 2666
; TYPE: DNA
; ORGANISM: *Oryza sativa*
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_90928C.1
US-10-437-963-92447

Query Match 80.8%; Score 242.4; DB 18; Length 2666;
Best Local Similarity 88.0%; Pred. No. 16-69; Indels 0; Gaps 0;
Matches 264; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 GATTATTGACAACACCGATCTGCTGGATTCATCAATTTGCTCACTAGACCTG 60
Db 1862 GATTATTGACAACACCGATCTGCTGGATTCATCAATTTGCTCACTAGACCTG 1803
QY 61 AACTGGCACTACTCTTGTATTTGTCAATTTCTTAAGCGGAGGCAACCTGAAACCCGCA 120
Db 1802 AACTGCACTACTCTTGTATTTGTATTTCAAGAGTGAAGGACACCTGAAACCCGCA 1743
QY 121 ATGGCTACTAGAAAGTACAGAAAGCCTTCAGAGATCGGGGGCTGCATTTCTGAAACAG 180
Db 1742 ATGGCTACTAGAAAGTACAGAAAGCCTTCAGAGATCGGGGGCTGCATTTCTGAAACAG 1683
QY 181 GTGTTCGAATTAATCAAGAAATTTCTGTGTGATTAACATCTGTAGAAATAGAGGATGT 240
Db 1682 GAGTTGCACTTACTCAAGAAATTTCTGTGTGATTAACATCTGTAGAAATAGAGGATGT 1623
QY 241 TAGCTCGGTTTCTTATTTGATTTGGTTGGTGTGATGATTCAGAAATGTCTGCTGTG 300
Db 1622 TAGCTGATTTTCCCATGTTTGAATGAGGTTGGTGAAGAACATCAAGAAATGTCACTGTG 1563

RESULT 10
US-10-767-701-27794
; Sequence 27794, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53335)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 27794
; LENGTH: 423
; TYPE: DNA
; ORGANISM: *Sorghum bicolor*
; FEATURE:
; OTHER INFORMATION: Clone ID: 721656
US-10-767-701-27794

Query Match 75.1%; Score 225.2; DB 18; Length 423;
Best Local Similarity 98.7%; Pred. No. 2.2e-64;
Matches 227; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATTATTGACAACACCGATCTGCTGGATTCATCAATTTGCTCACTAGACCTG 60
Db 194 GATTATTGACAACACCGATCTGCTGGATTCATCAATTTGCTCACTAGACCTG 253

Qy	Db	Qy	Db
6	254	121	314
AAATGGCACTACTCTGTAAATGTCATTTCAAGAGGAGGAGGACACCTGAAAACCGCA	AACTGGAACTACTCTGTAAATGTCATTTCAAGAGGAGGAGGACACCTGAAAACCGCA	ATGGTCTACAGAAAGTACAGAAAGCCCTCAGAGATGCGGGCGTGCAATTCTCGAAACAGG	ATGGTCTACAGAAAGTACAGAAAGCCCTCAGAGATGCGGGCGTGCAATTCTCGAAACAGG
120	313	180	373
181	374	230	423
GTGTTGCAATTACTCAAGAAATTTCTCTGTGGATPAACCTGCGAATA	GTGTTGCAATTACTCAAGAAATTTCTCTGTGGATPAACCTGCGAATA		

```

RESULT 11
US-10-767-795-1472
; Sequence 1472, Application US/10767795
; Publication No. US20040181830A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53534)B
; CURRENT APPLICATION NUMBER: US/10/767,795
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 1472
; LENGTH: 1491
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURES:
; OTHER INFORMATION: Clone ID: GOSH1-09MAY01-C1260_1
; US-10-767-795-1472

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Query Match	72.8%	Score 218.4	DB 18	Length 1491
Best Local Similarly	83.0%	Pred. No. 7.8e-62		
Matches 249; Conservative		0; Mismatches 51	Indels 0	Gaps 0

Qy	1	GATTATTATACAAACCAATCTGCTGGGATATGATCATCAAAATGGTCAATATAGAACCTG	60
Db	71	GATTATTATGATTAACAGATCCTGCTGGAAATGATCATCAAAATATAGACAACTTGGGCTG	130
Qy	61	AACTCGCACCTACTCTTGTATTTGTCATTTCTAAGCGGAGGCAACCTGAAACCCGCA	120
Db	131	AGTTGGCTTCTACTCTTGTATTTGATTTCAAAAGATGAGAGATACCCCTGAAACAAGAA	190
Qy	121	ATGGTCTACATAGAGATACAGAAAGCCTTCAGAGATGGGGGCTGCATTTCTCGAAACAGG	180
Db	191	ATGGTCTATTTGGAAGACAGAAAGCCCTTCGGAAGCTGGTCTGGATTTTGCAAAACAGG	250
Qy	181	GTGTTGCCAATTACTCAGAAAAATTTCTGTGGATATACACTGTAGATAGAGGATGCT	240
Db	251	GTGTGCTATTAACACAAGAAAATTTCTGTGGACAACACTGCAGAGATTAGGGTTGGG	310
Qy	241	TACCTGGTTTCTATGTTGATTTGGGTGGTGGTAGACATTCAGAAATGTCTGCTGG	300
Db	311	TACCAAGTTCCTATGTTGATTTGGGTGGGAGAGACCTCTGAAATGTCTCAATTTG	370

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RESULT 12
US-10-425-114-9307
; Sequence 9307, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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: FILE REFERENCE: 38-21(53313)B
: CURRENT APPLICATION NUMBER: US/10/425,114
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 9307
: LENGTH: 1411
: TYPE: DNA
: ORGANISM: Glycine max
: FEATURE:
: OTHER INFORMATION: Clone ID: 700845275_FLI
: US-10-425-114-9307

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	Query Match	Best Local Similarity	61.0%;	Score 208.8;	DB 17;	Length 1411;				
	Matches	243;	Conservative	0;	Mismatches	57;	Indels	0;	Gaps	0;
QY	1	GATTATTGCAACACCCGATCTTCCTGGGATTGATCATCTCAAAATGCTCAACTGAGACCTG	60							
Db	24	GATTGTGGCAACACCGATCTTCGCGAAATGATCATCTCAAGATTGCAACACTTGGGCGCTG	83							
QY	61	AACTGGCACTACTCTCTGTATATGTCAATTTCTAAGACGGAGGACACCTGMAACCCGCA	120							
Db	84	AGCTAGCTTCAACCTTGTGATTGTGATTCAAAGATGGAGGTACTCTGAGACCGAA	143							
QY	121	ATGCTCTACTAGAAGTACAGAAAGCCTTCAGAGATGGGGGCTGCATTTCTCGAAACAG	180							
Db	144	ATGGTTTATTTAGGAAGTCAGAAAGCCTTTGTGTAAAGACGCTTGATTTTCTTAAACAG	203							
QY	181	GTTGTGCAATTACTCAGAAAAATTCCTGTGTGATTAACACTGTGTAATAAGAGGATGT	240							
Db	204	GTGTGTCTATTAACAGAAAAATCTTTTGTGATTAACACTGCACGAATTAGGGCTGTGT	263							
QY	241	TAGCTCGCTTCCATGCTTTGATTGGTGTGTGATAGCACTTCAGAAATGTCTGCTGTG	300							
Db	264	TAGCTCAATTTCCATGCTTTGATTGGTGTGTGAGGTAAAGTCAAGATGTCTGCAGTTG	323							

RESULT 13
US-10-425-114-29640
; Sequence 29640, Application US/10425114
; Publication No. US20040034888A1

APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53313)B
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 29640
 LENGTH: 2218
 TYPE: DNA
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: UC-GMFMINSOY100E04_FLI
 US-10-425-114-29640

Query Match	69.6%	Score 208.8	DB 17	Length 2218
Best Local Similarity	81.0%	Pred. No. 1.5e-58		
Matches 243; Conservative	0	Mismatches 57	Indels 0	Gaps 0

Qy	Db	Qy	Db
1	775	61	835
GATTATTGGCAACCCGATCTCGTGGATTATCATCAAAATGCTCAACTGGACCTG	GATTGTGGACAACACGGATCTCGTGGATTGATCATCAGATTGGCACAACTTGGGGCTG	AACCTGGCAACTACTCTTGTAAATGTCAATTTCTAAGACGGAGCACACTGAAAACCCGCA	AGCTAGCTTTCAACACTTGTATTTGTGAATATCAAGATGAGAGTACTCTTGAGACCGAAA
60	834	120	894

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QY 121 ATGCTACTAGAGTACAGAAAGCCCTTCAGAGTGGGGGCTGCATTTCTCGAAACAG 180
Db 895 ATGCTTTATGGAAGTGCAGAAAGCCCTTCTGTGAGAGGCTTGATTTCTTAACAG 954
QY 181 GTGTTGCAATTACTCAAGAAATTTCTGTGTGATTAACACTGCTAGAAATAGAGGATGT 240
Db 955 GTGTTCTATTAACAAGAAATTTCTTGTGTGATTAACACTGCAAGATTTAGAGGCTGT 1014
QY 241 TAGCTGGTTTCTATGTTGATTTGGTTGGTGTAGGACTTCAAGAAATGCTGTGTG 300
Db 1015 TAGCTAGATTTCTATGTTGATTTGGTGGAGGTAGAAAGTCAAGATGCTGCAAGTTG 1074

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RESULT 14

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US-10-424-599-11100
/ Sequence 11100, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongmei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
/ FILE REFERENCE: 38-21(53223) B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 11100
/ LENGTH: 2547
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ LOCATION: (1) (2547)
/ OTHER INFORMATION: unsure at all n locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_110030C.1
US-10-424-599-11100

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Query Match      69.6%; Score 208.8; DB 17; Length 2547;
Best Local Similarity 81.0%; Pred. No. 1,6e-58;
Matches 243; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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QY 1 GATTTATTGACAACACCGATCCTGCTGAGATTGATCATCAAAATGCTCAACTAGAGCCTG 60
Db 1022 GATTTGTGACAACACCGATCCTGCTGAGATTGATCATCAAAATGCTCAACTAGAGCCTG 1081
QY 61 AACTGGCAACTACTCTTGTAAATTGTCATTTCTTAAGACGGAGGCAACCTGAAACCCGCA 120
Db 1082 AGCTAGCTTCAACACTTGTGATTTGATATCAAAAGTGAAGTACTCTCTGAGACAGAA 1141
QY 121 ATGCTCTACTAGAGTACAGAAAGCCCTTCAGAGATCGGGGGCTGCATTTCTGAAACAG 180
Db 1142 ATGCTTTATGGAAGTGCAGAAAGCCCTTCTGTGAGAGAGGCTTGTGATTTCTTAACAG 1201
QY 181 GTGTTGCAATTACTCAAGAAATTTCTGTGTGATTAACACTGCTAGAAATAGAGGATGT 240
Db 1202 GTGTTGCTATTAACAAGAAATTTCTTGTGTGATTAACACTGCAAGATTTAGAGGCTGT 1261
QY 241 TAGCTGGTTTCTATGTTGATTTGGTTGGTGTAGGACTTCAAGAAATGCTGTGTG 300
Db 1262 TAGCTAGATTTCTATGTTGATTTGGTGGAGGTAGAAAGTCAAGATGCTGCAAGTTG 1321

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RESULT 15

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US-09-938-842A-1222
/ Sequence 1222, Application US/09938842A
/ Patent No. US20020160378A1
/ GENERAL INFORMATION:
/ APPLICANT: Harper, Jeff
/ APPLICANT: Kreps, Joel

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/ APPLICANT: Wang, Xun
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
/ FILE REFERENCE: SCRIPI300-3
/ CURRENT APPLICATION NUMBER: US/09/938,842A
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR FILING DATE: 2001-06-22
/ NUMBER OF SEQ ID NOS: 5379
/ SEQ ID NO 1222
/ LENGTH: 1836
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-09-938-842A-1222

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Query Match      65.9%; Score 197.6; DB 9; Length 1836;
Best Local Similarity 78.7%; Pred. No. 7,6e-55;
Matches 236; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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QY 1 GATTTATTGACAACACCGATCCTGCTGAGATTGATCATCAAAATGCTCAACTAGAGCCTG 60
Db 641 GATTTATTGACAACACCGATCCTGCTGAGATTGATCATCAAAATGCTCAACTAGAGCCTG 700
QY 61 AACTGGCAACTACTCTTGTAAATTGTCATTTCTTAAGACGGAGGCAACCTGAAACCCGCA 120
Db 701 AGCTGGCTCGACTTATGATTTGTCATCTCAAGAGTGAAGTACTCTGAAACTAGAA 760
QY 121 ATGCTCTACTAGAGTACAGAAAGCCCTTCAGAGATCGGGGGCTGCATTTCTGAAACAG 180
Db 761 ATGACTACTGGAAGTACAGAAAGCATTCGTGAAGCTGTCTGATTTCCCAAAACAG 820
QY 181 GTGTTGCAATTACTCAAGAAATTTCTGTGTGATTAACACTGCTAGAAATAGAGGATGT 240
Db 821 GTGTTGCAATTACTCAAGAAATTTCTGTGTGATTAACACTGCTAGAAATAGAGGATGT 880
QY 241 TAGCTGGTTTCTATGTTGATTTGGTTGGTGTAGGACTTCAAGAAATGCTGTGTG 300
Db 881 TAGCTAGATTTCTATGTTGATTTGGTGGAGGTAGAAAGTCAAGATGCTGCAAGTTG 940

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Search completed: May 4, 2005, 21:11:52
Job time : 341.366 secs

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